SEQUENCE LISTING

<110> Mackenzie, Sally
Abdelnoor, Ricardo

<120> Implementation of a Mitochondrial Mutator

<130> 1231-218

<150> 60/456,318
<151> 2003-03-20

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<170> PatentIn version 3.2

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Met His Trp Ile Ala Thr Arg Asn Ala Val Val Ser Phe Pro Lys
1 5 10 15

tgg cgg ttc ttc ttc cgc tcc tca tat cgc act tac tct tcc ctc aaa 216
Trp Arg Phe Phe Phe Arg Ser Ser Tyr Arg Thr Tyr Ser Ser Leu Lys
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Pro Ser Ser Pro Ile Leu Leu Asn Arg Arg Tyr Ser Glu Gly Ile Ser
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Cys Leu Arg Asp Gly Lys Ser Leu Lys Arg Ile Thr Thr Ala Ser Lys
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Val Gly Glu Phe Tyr Glu Ala Ile Gly Ile Asp Ala Cys Ile Leu Val
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Glu Tyr Ala Gly Leu Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile
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cca aag gct ggc tgc cca att atg aat ctt cga cag act ttg gat gac      696
Pro Lys Ala Gly Cys Pro Ile Met Asn Leu Arg Gln Thr Leu Asp Asp
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Leu Thr Arg Asn Gly Tyr Ser Val Cys Ile Val Glu Glu Val Gln Gly
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His Pro Gly Ser Pro Tyr Val Tyr Gly Leu Val Gly Val Asp His Asp
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Gly Glu Cys Ser Ser Arg Asn Phe Glu Trp Phe Glu Gly Asp Thr Leu
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tcc gag ctc tta tca agg gtc aaa gat gtt tat ggt ctt gat gat gaa     1176
Ser Glu Leu Leu Ser Arg Val Lys Asp Val Tyr Gly Leu Asp Asp Glu
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att gct ctg aaa att caa gaa acg tgc aag ctc atg agc aca gta aca      1416
Ile Ala Leu Lys Ile Gln Glu Thr Cys Lys Leu Met Ser Thr Val Thr
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Glu Ile Leu Lys Leu Leu Met Asp Pro Thr Trp Val Ala Thr Gly Leu
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aaa att gac ttt gac act ttt gtc aac gaa tgt cat tgg gcg tct gat      1656
Lys Ile Asp Phe Asp Thr Phe Val Asn Glu Cys His Trp Ala Ser Asp
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Thr Ile Gly Glu Met Ile Ser Leu Asp Glu Asn Glu Ser His Gln Asn
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Val Ser Lys Cys Asp Asn Val Pro Asn Glu Phe Phe Tyr Asp Met Glu
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Ser Ser Trp Arg Gly Arg Val Lys Gly Ile His Ile Glu Glu Glu Ile
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act caa gta gaa aaa tca gct gag gct tta tct tta gca gta gct gag      1848
Thr Gln Val Glu Lys Ser Ala Glu Ala Leu Ser Leu Ala Val Ala Glu
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Lys Lys Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ile Ala
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Glu Leu Leu Arg Glu Leu Ser Val Lys Leu Gln Thr Lys Ile Asn Val
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Leu Val Phe Ala Ser Met Leu Leu Val Ile Ser Lys Ala Leu Phe Ser
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His Ala Cys Glu Gly Arg Arg Arg Lys Trp Val Phe Pro Thr Leu Val
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Gly Phe Ser Leu Asp Glu Gly Ala Lys Pro Leu Asp Gly Ala Ser Arg
720                 725                 730                 735

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Met Lys Leu Thr Gly Leu Ser Pro Tyr Trp Phe Asp Val Ser Ser Gly
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Ala Ala Leu Leu Gly Ile Ser Gly Leu Met Val Pro Ala Glu Ser Ala
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Cys Ile Pro His Phe Asp Ser Ile Met Leu His Met Lys Ser Tyr Asp
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Ser Pro Val Asp Gly Lys Ser Ser Phe Gln Val Glu Met Ser Glu Ile
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cga tct att gta agc cag gct act tcg aga agc cta gtg ctt ata gat     2664
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Thr His Leu His Gly Ile Phe Ser Leu Pro Leu Thr Ala Lys Asn Ile
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Ile Val Lys Ile Cys Gly Lys Lys Met  Ile Glu Pro Glu Ala  Ile Glu
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Cys Leu Ser  Ile Gly Ala Arg Glu  Leu Pro Pro Pro Ser  Thr Val
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Gly Ser Ser  Cys Val Tyr Val Met  Arg Arg Pro Asp Lys  Arg Leu
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Tyr Ile Gly  Gln Thr Asp Asp Leu  Glu Gly Arg Ile Arg  Ala His
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cga gca aag  gaa gga ctg caa ggg  tca agt ttt cta tac  ctt atg      3324
Arg Ala Lys  Glu Gly Leu Gln Gly  Ser Ser Phe Leu Tyr  Leu Met
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65                  70                  75                  80


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Tyr Ala Gly Leu Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro
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ttgaacccgt catcttatca agactgattc tgcgccgacc tttgcgactc cacggagcac 180

aattctatgg tgctattgca atatatgcct gcatacacgt ctgcatatgc tggtctcatc 240

gcgttttgga ggtcttctca tcagatacct atccagaggc tggctgccca attatggtac 300

acaatccttt ttgaatttca agctgcagcc cgggccgtcg accacgcgtg cccttagttg 360

agtcgtat 368

<210> 6
<211> 703
<212> DNA
<213> Hordeum vulgare

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (7)..(7)
<223> n is a, c, g, or t

<400> 6
gnacggnaaa gtcctttgac tggtttgatg gttctcctat tgacgaactt ttatgcaagg 60

taagggagat atatggcctg gacgagaaaa ctagtttccg caacgtcact atctcgttgg 120

aagggaggcc tcaaccttta tatcttggaa ctgctactca aattggagtg atatcaactg 180

aggggatccc cagtttacca aaaatgctac tccctccaaa ttgtgccggg cttccgtcaa 240

tgtatattag agatcttctt cttaatcctc catcttttga tgttgcctct gcaattcaag 300

aggcttgcag gcttatgtgc agcataactt gttcaattcc agaatttacc tgcataccat 360

cagcgaagct tgtgaaacta cttgagtcga aagaggttaa tcacatcgaa ttttgtagaa 420

taaaaaatgt ccttgacgag attatgttga tgaatggaat cactgagctt tcagctatcc 480

agaacaaatt gctcgaacct gcttcggtgg ttactggctt gaaagttgat gctgatatac 540

taattaaaga atgtagattt atttcgaaac gtataggtga agtgatatct ttagctggcg 600

aaagtgacca ggcaatatct tcatcggaat atattcccaa ggagttcttc aatgatatgg 660

agtcatcttg gaaggggccg tgtgaaaagg gtccatgctg aag 703

<210> 7
<211> 232
<212> PRT
<213> Hordeum vulgare

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<400> 7

Thr Xaa Lys Ser Phe Asp Trp Phe Asp Gly Ser Pro Ile Asp Glu Leu
1 5 10 15

Leu Cys Lys Val Arg Glu Ile Tyr Gly Leu Asp Glu Lys Thr Ser Phe
20 25 30

Arg Asn Val Thr Ile Ser Leu Glu Gly Arg Pro Gln Pro Leu Tyr Leu
35 40 45

Gly Thr Ala Thr Gln Ile Gly Val Ile Ser Thr Glu Gly Ile Pro Ser
50 55 60

Leu Pro Lys Met Leu Leu Pro Pro Asn Cys Ala Gly Leu Pro Ser Met
65 70 75 80

Tyr Ile Arg Asp Leu Leu Leu Asn Pro Pro Ser Phe Asp Val Ala Ser

85 90 95

Ala Ile Gln Glu Ala Cys Arg Leu Met Cys Ser Ile Thr Cys Ser Ile
100 105 110

Pro Glu Phe Thr Cys Ile Pro Ser Ala Lys Leu Val Lys Leu Leu Glu
115 120 125

Ser Lys Glu Val Asn His Ile Glu Phe Cys Arg Ile Lys Asn Val Leu
130 135 140

Asp Glu Ile Met Leu Met Asn Gly Ile Thr Glu Leu Ser Ala Ile Gln
145 150 155 160

Asn Lys Leu Leu Glu Pro Ala Ser Val Val Thr Gly Leu Lys Val Asp
165 170 175

Ala Asp Ile Leu Ile Lys Glu Cys Arg Phe Ile Ser Lys Arg Ile Gly
180 185 190

Glu Val Ile Ser Leu Ala Gly Glu Ser Asp Gln Ala Ile Ser Ser Ser
195 200 205

Glu Tyr Ile Pro Lys Glu Phe Phe Asn Asp Met Glu Ser Ser Trp Lys
210 215 220

Gly Pro Cys Glu Lys Gly Pro Cys
225 230

<210> 8
<211> 540
<212> DNA
<213> Hordeum vulgare

<400> 8
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caacaggttc ttttggactg ctgcgaaagg atgtcgagag cattgttact gcgatatgcg 120

aagacaagct gttggacctg tacaacaaga gaagcatctc agagcagatt gaggtggtct 180

gtgtaactgt aggtgctagg gagcaaccgc caccttcaac cgttggcagg tccagcatct 240

atatcattat cagacgtgac aacaagctct atgttggaca gacggatgat ctcgtgggcc 300

gtcttggtgc tcatagatcc aaggaaggta tgcaagatgc cacaatatta tacatcgtgg 360

ttcctggcaa gagcgttgcg tgccaactgg agactcttct cataaatcag ctaccctcga 420

aaggttttaa gctcaccaac aaggcagatg gcaagcatcg gaactttggt atgtctgtaa 480

cctctggaga agccatggcc gcgcactgaa ctgccccact gaacatccag ttttaactcg 540

<210> 9
<211> 168
<212> PRT
<213> Hordeum vulgare

<400> 9

Ser Val Asn Gly Gly Leu Val Asp Arg Pro Asp Gly Leu Gly Asn Gly
1 5 10 15

Leu Glu Pro Pro Thr Gly Ser Phe Gly Leu Leu Arg Lys Asp Val Glu
20 25 30

Ser Ile Val Thr Ala Ile Cys Glu Asp Lys Leu Leu Asp Leu Tyr Asn
35 40 45

Lys Arg Ser Ile Ser Glu Gln Ile Glu Val Val Cys Val Thr Val Gly
50 55 60

Ala Arg Glu Gln Pro Pro Pro Ser Thr Val Gly Arg Ser Ser Ile Tyr
65 70 75 80

Ile Ile Ile Arg Arg Asp Asn Lys Leu Tyr Val Gly Gln Thr Asp Asp
85 90 95

Leu Val Gly Arg Leu Gly Ala His Arg Ser Lys Glu Gly Met Gln Asp
100 105 110

Ala Thr Ile Leu Tyr Ile Val Val Pro Gly Lys Ser Val Ala Cys Gln
115 120 125

Leu Glu Thr Leu Leu Ile Asn Gln Leu Pro Ser Lys Gly Phe Lys Leu
130 135 140

Thr Asn Lys Ala Asp Gly Lys His Arg Asn Phe Gly Met Ser Val Thr
145 150 155 160

Ser Gly Glu Ala Met Ala Ala His
165

<210> 10
<211> 540
<212> DNA
<213> Hordeum vulgare

<400> 10
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caacaggttc ttttggactg ctgcgaaagg atgtcgagag cattgttact gcgatatgcg 120

aagacaagct gttggacctg tacaacaaga gaagcatctc agagcagatt gaggtggtct 180

gtgtaactgt aggtgctagg gagcaaccgc caccttcaac cgttggcagg tccagcatct 240

atatcattat cagacgtgac aacaagctct atgttggaca gacggatgat ctcgtgggcc 300

gtcttggtgc tcatagatcc aaggaaggta tgcaagatgc cacaatatta tacatcgtgg 360

ttcctggcaa gagcgttgcg tgccaactgg agactcttct cataaatcag ctaccctcga 420

aaggttttaa gctcaccaac aaggcagatg gcaagcatcg gaactttggt atgtctgtaa 480

cctctggaga agccatggcc gcgcactgaa ctgccccact gaacatccag ttttaactcg 540

<210> 11
<211> 444
<212> DNA
<213> Zea mays

<400> 11
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ctagcaccac tatcagttca acaaaactag ggcggcatgg tgtcagttag ctcccgcctc 120

ctattgaata tccaatagca aaaagacctt cagctgacta gttccgtcga gtagcaactg 180

cctcgccaga gattcgagat ataccgaagt tcctgtgctt cccgtctgcc ttgttgatga 240

gcttgaagcc cctcgaaggg agctggttta tgagaagggt ttccagctgg caggcaacgc 300

tcttgccagg gaccaagacg tataataccg tagcgtcccg catgccttcc ttcgatctgt 360

gggcgttcaa gcgccccaga agatcgtccg tctgtccaac atagagcctg ttgtcgcttc 420

tgataatcac gtagatgcta gatc 444

<210> 12
<211> 94
<212> PRT
<213> Zea mays

<400> 12

Ser Ser Ile Tyr Val Ile Ile Arg Ser Asp Asn Arg Leu Tyr Val Gly
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Gln Thr Asp Asp Leu Leu Gly Arg Leu Asn Ala His Arg Ser Lys Glu
20 25 30

Gly Met Arg Asp Ala Thr Val Leu Tyr Val Leu Val Pro Gly Lys Ser
35 40 45

Val Ala Cys Gln Leu Glu Thr Leu Leu Ile Asn Gln Leu Pro Ser Arg
50 55 60

Gly Phe Lys Leu Ile Asn Lys Ala Asp Gly Lys His Arg Asn Phe Gly
65 70 75 80

Ile Ser Arg Ile Ser Gly Glu Ala Val Ala Thr Arg Arg Asn
85 90

<210> 13
<211> 338
<212> DNA
<213> Medicago truncatula

<400> 13
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ggagggaatc tctttagcta atccaattga agtttcacat aaggaggttg agagtgctat 120

cactgtaatc tgccaagatt ttatagcgga actgcgaagg aaaaagatca catcataact 180

tatcaagata aagtgtttct taattggcac tagggaatgg ccacctccga tgactatatg 240

ctcttcaagt gtctacgtga tgctcagacc agatcagaaa ctctacgtag gagagacgga 300

taatctcgag gatcgagttc gtgcacatcg atcgaaag 338

<210> 14
<211> 679
<212> DNA
<213> Allium cepa

<400> 14
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tgacaaagct gctcagtctt tgtctattac agttatggaa gactttgttc caatcgtttc 120

tagagtaaaa gcggttatgt cttctcttgg aggtccaaag ggtgaagtat gttatgctag 180

agaacatgaa gctgtttggt tcaaaggaaa gcgttttatg ccatctgttt gggctaatac 240

acctggggaa gagcagatca agaaacttaa acctgccttg gattcaaaag gaagaaaagt 300

cggagaggaa tggttcacaa cgatcaatat tgagaatgca ttaactaggt atcatgaatc 360

tacggaaaag gcaagaatta aagttttgga cttattaaga gaactttctg gagaaatgca 420

ggctaaaatt aacatccttg tcttctcttc catgctgctt gtcatatcta aatctctttt 480

tggccatgtt agtgaaggta ggagaagagg atgggtgttt cctgacctgc acaattccca 540

aatcataagg ataatagttt ggacactggt aatgaaacac ttgagctaag agatttatca 600

cctttatggt ttgatgctgt gcaaggaagt gcaatggaaa atactgtcag aatgcattct 660

atgtttcttt tactgggcc 679

<210> 15
<211> 179
<212> PRT
<213> Allium cepa

<400> 15

Glu Ser Ser Trp Lys Gly Arg Val Lys Arg Ile His Ala Glu Asp Val

1 5 10 15

Phe Ala Glu Val Asp Lys Ala Ala Gln Ser Leu Ser Ile Thr Val Met
20 25 30

Glu Asp Phe Val Pro Ile Val Ser Arg Val Lys Ala Val Met Ser Ser
35 40 45

Leu Gly Gly Pro Lys Gly Glu Val Cys Tyr Ala Arg Glu His Glu Ala
50 55 60

Val Trp Phe Lys Gly Lys Arg Phe Met Pro Ser Val Trp Ala Asn Thr
65 70 75 80

Pro Gly Glu Glu Gln Ile Lys Lys Leu Lys Pro Ala Leu Asp Ser Lys
85 90 95

Gly Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Ile Asn Ile Glu Asn
100 105 110

Ala Leu Thr Arg Tyr His Glu Ser Thr Glu Lys Ala Arg Ile Lys Val
115 120 125

Leu Asp Leu Leu Arg Glu Leu Ser Gly Glu Met Gln Ala Lys Ile Asn
130 135 140

Ile Leu Val Phe Ser Ser Met Leu Leu Val Ile Ser Lys Ser Leu Phe
145 150 155 160

Gly His Val Ser Glu Gly Arg Arg Arg Gly Trp Val Phe Pro Asp Leu
165 170 175

His Asn Ser

<210> 16
<211> 662
<212> DNA
<213> Citrus sinensis

<400> 16
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cttcgttact tggcatatgt ggtcttatgg tgcccgcaga gtcagcctca attccttact 180

ttgatgctat catgcttcac atgaaatcct atgatagccc tgctgacggg aaaagctcat 240

ttcaggtatt ctggttcctt gtactgaggt tgtaagtttg ctcatgccat gatagatcga 300

gcttagccat gatcttgtga ggcatggtag tagtaactgg tgcaggtgag aaatgttgag 360

tactacaatt tacacattgc acttcacctc tcatctcaaa tctggtggaa aagcgtaatg 420

tattaatttt ctgtggatat tatatgtctg cattctctta atttcagtat ttgctgcaaa 480

aggttatctc cattaagttg cacatgttgc tcagtacctt aagtttttac tttgaacaag 540

caatttttg tatgttggaa ttatcttcga taggagtggt atcaagtaat atgcaaataa 600

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tt 662

<210> 17
<211> 81
<212> PRT
<213> Citrus sinensis

<400> 17

Trp Phe Asp Ala Ala Glu Gly Ser Ala Val His Asn Thr Val Asp Met
1 5 10 15

Gln Ser Leu Phe Leu Leu Thr Gly Pro Asn Gly Gly Gly Lys Ser Ser
20 25 30

Leu Leu Arg Ser Ile Cys Ala Ala Ser Leu Leu Gly Ile Cys Gly Leu
35 40 45

Met Val Pro Ala Glu Ser Ala Ser Ile Pro Tyr Phe Asp Ala Ile Met
50 55 60

Leu His Met Lys Ser Tyr Asp Ser Pro Ala Asp Gly Lys Ser Ser Phe
65 70 75 80

Gln

<210> 18
<211> 600
<212> DNA
<213> Solanum tuberosum

<400> 18
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acgtcgccgt ttcagttccc cgttggcgtt cactgtccct tttcctccgt ccaccacttc 120

gccggcgttt cttctctttc tctccacata ctctgtgccg agagcagata cgttgcttga 180

aggagcggaa gttttttgcc acaacggcaa aaaaaaactc aaacaaccaa aaagtgttcc 240

agaggaaaaa gactatgtta atattatgtg gtggaaagag agaatggaat tcttgagaaa 300

gccttcttct gttctactgg ctaagaggct tacatattgt aacttgctgg gtgtggatcc 360

gagtttgaga aatggaagtc ttaaagaggg aacacttaac tcggagatgt tgctgttcaa 420

gtcaaaattt cctcgtgaag ttttgttctg tagagtaggt gatttttatg aagcaattgg 480

attcgatgct tgtattcttg tggaatatgc tggtttaaat ccatttggtg gcctgcgctc 540

agatagtata ccaaaagctg gttgtccagt tgtgaatcta agacagacgt tggatgatct 600

<210> 19
<211> 187
<212> PRT
<213> Solanum tuberosum

<400> 19

Met Tyr Trp Val Thr Ala Lys Asn Val Ala Val Ser Val Pro Arg Trp
1 5 10 15

Arg Ser Leu Ser Leu Phe Leu Arg Pro Pro Leu Arg Arg Arg Phe Phe
20 25 30

Ser Phe Ser Pro His Thr Leu Cys Arg Glu Gln Ile Arg Cys Leu Lys
35 40 45

Glu Arg Lys Phe Phe Ala Thr Thr Ala Lys Lys Lys Leu Lys Gln Pro
50 55 60

Lys Ser Val Pro Glu Glu Lys Asp Tyr Val Asn Ile Met Trp Trp Lys
65 70 75 80

Glu Arg Met Glu Phe Leu Arg Lys Pro Ser Ser Val Leu Leu Ala Lys
85 90 95

Arg Leu Thr Tyr Cys Asn Leu Leu Gly Val Asp Pro Ser Leu Arg Asn
100 105 110

Gly Ser Leu Lys Glu Gly Thr Leu Asn Ser Glu Met Leu Leu Phe Lys
115 120 125

Ser Lys Phe Pro Arg Glu Val Leu Phe Cys Arg Val Gly Asp Phe Tyr
130 135 140

Glu Ala Ile Gly Phe Asp Ala Cys Ile Leu Val Glu Tyr Ala Gly Leu
145 150 155 160

Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro Lys Ala Gly Cys
165 170 175

Pro Val Val Asn Leu Arg Gln Thr Leu Asp Asp
180 185

<210> 20
<211> 3396
<212> DNA
<213> Oryza sativa

<400> 20
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ctgtggtgga aagagaaaat ggagaggtgc aggaaaccat catcaatgca attgactcag 300

agacttgtgt attcaaatat tttaggattg gatccaactt taagaaatgg aagcttgaag 360

gatggaagcc tgaacacgga aatgttgcaa ttcaaatcga agtttcctcg tgaagttcta 420

ctttgcagag tgggagattt ctacgaggct gttgggtttg atgcatgtat ccttgtggag 480

catgcaggct taaatccttt tggaggcttg cgttctgata gtattccaaa agctggatgt 540

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agaataaaga atgtcctcga tgaggtgttg ttcatgggta gcaatgctga gctttctgct 1440

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cagctacctt tgaaaggttt caagctcatc aacaaggcag atggcaagca tcgaaatttc 3360
ggtatatctc ttgtcccagg agaggcaatt gccgca 3396

<210> 21
<211> 3396
<212> DNA

<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(3396)

<400> 21

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Met Ala Ile Gln Arg Leu Leu Ala Ser Ser Leu Val Ala Ala Thr Pro
1               5                   10                  15

cgg tgg ctt ccc gtc gcc gcc gac tcg ttt ctc cgg cgc cgc cac cgc       96
Arg Trp Leu Pro Val Ala Ala Asp Ser Phe Leu Arg Arg Arg His Arg
            20                  25                  30

cct cgc tgc tcc ccg ctc ccc gcg ctg cta ttt aac agg agg tcc tgg      144
Pro Arg Cys Ser Pro Leu Pro Ala Leu Leu Phe Asn Arg Arg Ser Trp
        35                  40                  45

tct aaa cca agg aaa gtc tca cga agc att tcc att gtg tct agg aag      192
Ser Lys Pro Arg Lys Val Ser Arg Ser Ile Ser Ile Val Ser Arg Lys
    50                  55                  60

atg aac aaa caa gga gat ctc tgt aat gaa ggc atg ctg cca cat att      240
Met Asn Lys Gln Gly Asp Leu Cys Asn Glu Gly Met Leu Pro His Ile
65                  70                  75                  80

ctg tgg tgg aaa gag aaa atg gag agg tgc agg aaa cca tca tca atg      288
Leu Trp Trp Lys Glu Lys Met Glu Arg Cys Arg Lys Pro Ser Ser Met
                85                  90                  95

caa ttg act cag aga ctt gtg tat tca aat att tta gga ttg gat cca      336
Gln Leu Thr Gln Arg Leu Val Tyr Ser Asn Ile Leu Gly Leu Asp Pro
            100                 105                 110

act tta aga aat gga agc ttg aag gat gga agc ctg aac acg gaa atg      384
Thr Leu Arg Asn Gly Ser Leu Lys Asp Gly Ser Leu Asn Thr Glu Met
        115                 120                 125

ttg caa ttc aaa tcg aag ttt cct cgt gaa gtt cta ctt tgc aga gtg      432
Leu Gln Phe Lys Ser Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val
    130                 135                 140

gga gat ttc tac gag gct gtt ggg ttt gat gca tgt atc ctt gtg gag      480
Gly Asp Phe Tyr Glu Ala Val Gly Phe Asp Ala Cys Ile Leu Val Glu
145                 150                 155                 160

cat gca ggc tta aat cct ttt gga ggc ttg cgt tct gat agt att cca      528
His Ala Gly Leu Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro
                165                 170                 175

aaa gct gga tgt cca gtc atg aat ttg cgg cag aca ttg gat gat ttg      576
Lys Ala Gly Cys Pro Val Met Asn Leu Arg Gln Thr Leu Asp Asp Leu
            180                 185                 190

act cga tgt ggt tac tct gtg tgc ata gtt gaa gaa att caa ggc cca      624
Thr Arg Cys Gly Tyr Ser Val Cys Ile Val Glu Glu Ile Gln Gly Pro
        195                 200                 205

acc caa gct cgt gct agg aaa ggc cga ttt att tct ggc cat gca cat      672
Thr Gln Ala Arg Ala Arg Lys Gly Arg Phe Ile Ser Gly His Ala His
    210                 215                 220
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cct ggt agt cct tat gta ttt ggt ctt gct gaa gta gac cat gat gtt      720
Pro Gly Ser Pro Tyr Val Phe Gly Leu Ala Glu Val Asp His Asp Val
225                 230                 235                 240

gag ttc cct gat cca atg cct gta gtt ggg att tca cga tct gca aaa      768
Glu Phe Pro Asp Pro Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys
                245                 250                 255

ggc tat tgc ctg att tct gtg cta gag aca atg aaa aca tat tca gct      816
Gly Tyr Cys Leu Ile Ser Val Leu Glu Thr Met Lys Thr Tyr Ser Ala
            260                 265                 270

gag gag ggc tta aca gag gaa gca gtt gtt act aag ctt cgc ata tgc      864
Glu Glu Gly Leu Thr Glu Glu Ala Val Val Thr Lys Leu Arg Ile Cys
        275                 280                 285

cgt tat cat cat cta tac ctt cat agt tct ttg agg aac aat tct tca      912
Arg Tyr His His Leu Tyr Leu His Ser Ser Leu Arg Asn Asn Ser Ser
    290                 295                 300

ggc aca tca cgc tgg gga gaa ttt ggc gaa ggt ggg cta ttg tgg gga      960
Gly Thr Ser Arg Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly
305                 310                 315                 320

gag tgc agt gga aaa tct ttt gag tgg ttt gat ggt aat cct att gaa     1008
Glu Cys Ser Gly Lys Ser Phe Glu Trp Phe Asp Gly Asn Pro Ile Glu
                325                 330                 335

gaa ctg tta tgc aag gta agg gaa ata tat ggg ctt gaa gag aag act     1056
Glu Leu Leu Cys Lys Val Arg Glu Ile Tyr Gly Leu Glu Glu Lys Thr
            340                 345                 350

gtt ttc cgt aat gtc agt gtc tca ttg gaa ggg agg cct caa ccc ttg     1104
Val Phe Arg Asn Val Ser Val Ser Leu Glu Gly Arg Pro Gln Pro Leu
        355                 360                 365

tat ctt gga aca gct act caa att ggg gtg ata cca act gag gga ata     1152
Tyr Leu Gly Thr Ala Thr Gln Ile Gly Val Ile Pro Thr Glu Gly Ile
    370                 375                 380

ccc agt ttg cta aaa att gtt ctc cct cca aac ttt ggt ggc ctt cca     1200
Pro Ser Leu Leu Lys Ile Val Leu Pro Pro Asn Phe Gly Gly Leu Pro
385                 390                 395                 400

tca ttg tat att aga gat ctt ctt ctt aac cct cca tct ttt gat gtt     1248
Ser Leu Tyr Ile Arg Asp Leu Leu Leu Asn Pro Pro Ser Phe Asp Val
                405                 410                 415

gca tca tca gtt caa gag gct tgc agg ctt atg ggt agc ata act tgc     1296
Ala Ser Ser Val Gln Glu Ala Cys Arg Leu Met Gly Ser Ile Thr Cys
            420                 425                 430

tcg att cct gaa ttt aca tgc ata ccg gca gca aag ctt gtg aaa tta     1344
Ser Ile Pro Glu Phe Thr Cys Ile Pro Ala Ala Lys Leu Val Lys Leu
        435                 440                 445

ctc gag tca aaa gag gtt aat cac atc gaa ttt tgt aga ata aag aat     1392
Leu Glu Ser Lys Glu Val Asn His Ile Glu Phe Cys Arg Ile Lys Asn
    450                 455                 460

gtc ctc gat gag gtg ttg ttc atg ggt agc aat gct gag ctt tct gct     1440
Val Leu Asp Glu Val Leu Phe Met Gly Ser Asn Ala Glu Leu Ser Ala
```

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465                 470                 475                 480

atc ctg aat aaa ttg ctt gat cct gcc gcc ata gtt act ggg ttc aaa     1488
Ile Leu Asn Lys Leu Leu Asp Pro Ala Ala Ile Val Thr Gly Phe Lys
                485                 490                 495

gtt gaa gcc gat ata cta gtg aat gaa tgt agc ttt att tca caa cgt     1536
Val Glu Ala Asp Ile Leu Val Asn Glu Cys Ser Phe Ile Ser Gln Arg
            500                 505                 510

ata gct gaa gta atc tct tta ggt ggt gaa agt gac cag gca ata act     1584
Ile Ala Glu Val Ile Ser Leu Gly Gly Glu Ser Asp Gln Ala Ile Thr
        515                 520                 525

tca tct gaa tat att ccg aaa gag ttc ttc aat ggt atg gag tca tct     1632
Ser Ser Glu Tyr Ile Pro Lys Glu Phe Phe Asn Gly Met Glu Ser Ser
    530                 535                 540

tgg aag gga cgt gta aaa agg gtg cat gct gaa gag gag ttc tca aat     1680
Trp Lys Gly Arg Val Lys Arg Val His Ala Glu Glu Glu Phe Ser Asn
545                 550                 555                 560

gtt gat ata gct gct gag gca ctg tca aca gcg gtc att gaa gat ttt     1728
Val Asp Ile Ala Ala Glu Ala Leu Ser Thr Ala Val Ile Glu Asp Phe
                565                 570                 575

ctg cca att att tca aga gta aaa tct gtg atg tcc tca aat gga agt     1776
Leu Pro Ile Ile Ser Arg Val Lys Ser Val Met Ser Ser Asn Gly Ser
            580                 585                 590

tcg aag gga gaa atc agt tat gca aaa gag cat gaa tct gtt tgg ttt     1824
Ser Lys Gly Glu Ile Ser Tyr Ala Lys Glu His Glu Ser Val Trp Phe
        595                 600                 605

aaa ggg agg cga ttc aca cca aat gtg tgg gcc aac act cct ggt gaa     1872
Lys Gly Arg Arg Phe Thr Pro Asn Val Trp Ala Asn Thr Pro Gly Glu
    610                 615                 620

cta cag ata aag caa ttg aag cct gca att gac tca aaa ggt aga aag     1920
Leu Gln Ile Lys Gln Leu Lys Pro Ala Ile Asp Ser Lys Gly Arg Lys
625                 630                 635                 640

gtc gga gaa gaa tgg ttc acc act atc aaa gtt gag aat gct tta acc     1968
Val Gly Glu Glu Trp Phe Thr Thr Ile Lys Val Glu Asn Ala Leu Thr
                645                 650                 655

agg tac cat gaa gct tgt gat aat gca aaa cgt aaa gtt ctt gag ttg     2016
Arg Tyr His Glu Ala Cys Asp Asn Ala Lys Arg Lys Val Leu Glu Leu
            660                 665                 670

ttg aga gga ctt tca agt gaa ttg cag gac aag att aat gtc ctt gtc     2064
Leu Arg Gly Leu Ser Ser Glu Leu Gln Asp Lys Ile Asn Val Leu Val
        675                 680                 685

ttt tgc tca acg atg ctc atc ata aca aaa gca ctt ttt ggt cat gtt     2112
Phe Cys Ser Thr Met Leu Ile Ile Thr Lys Ala Leu Phe Gly His Val
    690                 695                 700

agt gaa gga cga aga agg ggt tgg gtg ctt cct act ata tct ccc ttg     2160
Ser Glu Gly Arg Arg Arg Gly Trp Val Leu Pro Thr Ile Ser Pro Leu
705                 710                 715                 720

tgt aag gat aat gtt aca gag gaa atc tca agt gaa atg gaa ttg tca     2208
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Cys Lys Asp Asn Val Thr Glu Glu Ile Ser Ser Glu Met Glu Leu Ser
                725                 730                 735

gga act ttt cct tac tgg ctt gat act aac caa ggg aat gca ata ctg     2256
Gly Thr Phe Pro Tyr Trp Leu Asp Thr Asn Gln Gly Asn Ala Ile Leu
            740                 745                 750

aat gat gtc cat atg cac tct ttg ttt att ctt act ggt cca aac ggt     2304
Asn Asp Val His Met His Ser Leu Phe Ile Leu Thr Gly Pro Asn Gly
        755                 760                 765

ggt ggt aaa tcc agt atg ctg aga tca gtc tgt gct gct gca tta ctt     2352
Gly Gly Lys Ser Ser Met Leu Arg Ser Val Cys Ala Ala Ala Leu Leu
    770                 775                 780

gga ata tgt ggc ctg atg gtg cca gct gct tca gct gtc atc cca cat     2400
Gly Ile Cys Gly Leu Met Val Pro Ala Ala Ser Ala Val Ile Pro His
785                 790                 795                 800

ttc gat tcc atc atg ctg cat atg aaa gca tat gat agc cca gct gat     2448
Phe Asp Ser Ile Met Leu His Met Lys Ala Tyr Asp Ser Pro Ala Asp
                805                 810                 815

ggt aaa agt tcg ttt cag att gaa atg tca gag ata cga tct tta gtc     2496
Gly Lys Ser Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Val
            820                 825                 830

tgc cga gct aca gct agg agt ctt gtt cta att gat gaa ata tgt agg     2544
Cys Arg Ala Thr Ala Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg
        835                 840                 845

ggc aca gaa aca gca aaa gga aca tgt ata gct ggt agc atc att gaa     2592
Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Ile Ile Glu
    850                 855                 860

aga ctc gat aat gtt ggc tgc ata ggc atc ata tca act cat ttg cat     2640
Arg Leu Asp Asn Val Gly Cys Ile Gly Ile Ile Ser Thr His Leu His
865                 870                 875                 880

ggc att ttt gac ctt cca ctg tca ctc cac aat act gat ttc aaa gct     2688
Gly Ile Phe Asp Leu Pro Leu Ser Leu His Asn Thr Asp Phe Lys Ala
                885                 890                 895

atg gga acc gaa atc atc gat agg tgc att cag cca aca tgg aaa tta     2736
Met Gly Thr Glu Ile Ile Asp Arg Cys Ile Gln Pro Thr Trp Lys Leu
            900                 905                 910

atg gat ggc atc tgt aga gag agt ctt gct ttt caa aca gcc agg aaa     2784
Met Asp Gly Ile Cys Arg Glu Ser Leu Ala Phe Gln Thr Ala Arg Lys
        915                 920                 925

gaa ggt atg cct gac ttg ata att aga aga gct gag gaa cta tat ttg     2832
Glu Gly Met Pro Asp Leu Ile Ile Arg Arg Ala Glu Glu Leu Tyr Leu
    930                 935                 940

gct atg agc aca aac agc aag cat aca tca tca gct gtc cac cat gaa     2880
Ala Met Ser Thr Asn Ser Lys His Thr Ser Ser Ala Val His His Glu
945                 950                 955                 960

ata tcc ata gcc aac tct act gta aat agc ttg gtt gag aag cct aat     2928
Ile Ser Ile Ala Asn Ser Thr Val Asn Ser Leu Val Glu Lys Pro Asn
                965                 970                 975
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tac ctg aga aat gga cta gag ctt caa tct ggt tcc ttc gga tta cta     2976
Tyr Leu Arg Asn Gly Leu Glu Leu Gln Ser Gly Ser Phe Gly Leu Leu
            980                 985                 990

aga aaa gaa att gag agt gtt gtt  acc aca ata tgc aag  aag aaa ctg   3024
Arg Lys Glu Ile Glu Ser Val Val  Thr Thr Ile Cys Lys  Lys Lys Leu
        995                 1000                1005

ttg gat  ctc tac aac aaa agg  agc atc tca gaa ctg  att gag gtg      3069
Leu Asp  Leu Tyr Asn Lys Arg  Ser Ile Ser Glu Leu  Ile Glu Val
    1010                1015                1020

gtc tgt  gtt gct gtg ggt gct  agg gag caa ccc cca  cct tca act      3114
Val Cys  Val Ala Val Gly Ala  Arg Glu Gln Pro Pro  Pro Ser Thr
    1025                1030                1035

gtt ggc  agg tcc agc att tat  gta att atc aga cgt  gac agc aag      3159
Val Gly  Arg Ser Ser Ile Tyr  Val Ile Ile Arg Arg  Asp Ser Lys
    1040                1045                1050

ctc tat  att gga cag acg gat  gat ctt gtg ggt cga  ctt agt gct      3204
Leu Tyr  Ile Gly Gln Thr Asp  Asp Leu Val Gly Arg  Leu Ser Ala
    1055                1060                1065

cac aga  tcg aag gaa ggt atg  cag gat gcc acg ata  tta tat att      3249
His Arg  Ser Lys Glu Gly Met  Gln Asp Ala Thr Ile  Leu Tyr Ile
    1070                1075                1080

ttg gta  cct ggg aag agc att  gca tgc caa ctg gaa  act ctt ctc      3294
Leu Val  Pro Gly Lys Ser Ile  Ala Cys Gln Leu Glu  Thr Leu Leu
    1085                1090                1095

ata aat  cag cta cct ttg aaa  ggt ttc aag ctc atc  aac aag gca      3339
Ile Asn  Gln Leu Pro Leu Lys  Gly Phe Lys Leu Ile  Asn Lys Ala
    1100                1105                1110

gat ggc  aag cat cga aat ttc  ggt ata tct ctt gtc  cca gga gag      3384
Asp Gly  Lys His Arg Asn Phe  Gly Ile Ser Leu Val  Pro Gly Glu
    1115                1120                1125

gca att  gcc gca                                                  3396
Ala Ile  Ala Ala
    1130
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<210> 22
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<213> Oryza sativa

<400> 22

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Arg Trp Leu Pro Val Ala Ala Asp Ser Phe Leu Arg Arg Arg His Arg
            20                  25                  30

Pro Arg Cys Ser Pro Leu Pro Ala Leu Leu Phe Asn Arg Arg Ser Trp
        35                  40                  45
```

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Ser Lys Pro Arg Lys Val Ser Arg Ser Ile Ser Ile Val Ser Arg Lys
    50                  55                  60

Met Asn Lys Gln Gly Asp Leu Cys Asn Glu Gly Met Leu Pro His Ile
65                  70                  75                  80

Leu Trp Trp Lys Glu Lys Met Glu Arg Cys Arg Lys Pro Ser Ser Met
                85                  90                  95

Gln Leu Thr Gln Arg Leu Val Tyr Ser Asn Ile Leu Gly Leu Asp Pro
            100                 105                 110

Thr Leu Arg Asn Gly Ser Leu Lys Asp Gly Ser Leu Asn Thr Glu Met
        115                 120                 125

Leu Gln Phe Lys Ser Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val
    130                 135                 140

Gly Asp Phe Tyr Glu Ala Val Gly Phe Asp Ala Cys Ile Leu Val Glu
145                 150                 155                 160

His Ala Gly Leu Asn Pro Phe Gly Gly Leu Arg Ser Asp Ser Ile Pro
                165                 170                 175

Lys Ala Gly Cys Pro Val Met Asn Leu Arg Gln Thr Leu Asp Asp Leu
            180                 185                 190

Thr Arg Cys Gly Tyr Ser Val Cys Ile Val Glu Glu Ile Gln Gly Pro
        195                 200                 205

Thr Gln Ala Arg Ala Arg Lys Gly Arg Phe Ile Ser Gly His Ala His
    210                 215                 220

Pro Gly Ser Pro Tyr Val Phe Gly Leu Ala Glu Val Asp His Asp Val
225                 230                 235                 240

Glu Phe Pro Asp Pro Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys
                245                 250                 255

Gly Tyr Cys Leu Ile Ser Val Leu Glu Thr Met Lys Thr Tyr Ser Ala
            260                 265                 270

Glu Glu Gly Leu Thr Glu Glu Ala Val Val Thr Lys Leu Arg Ile Cys
        275                 280                 285

Arg Tyr His His Leu Tyr Leu His Ser Ser Leu Arg Asn Asn Ser Ser
    290                 295                 300
```

```
Gly Thr Ser Arg Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly
305                 310                 315                 320

Glu Cys Ser Gly Lys Ser Phe Glu Trp Phe Asp Gly Asn Pro Ile Glu
                325                 330                 335

Glu Leu Leu Cys Lys Val Arg Glu Ile Tyr Gly Leu Glu Glu Lys Thr
            340                 345                 350

Val Phe Arg Asn Val Ser Val Ser Leu Glu Gly Arg Pro Gln Pro Leu
        355                 360                 365

Tyr Leu Gly Thr Ala Thr Gln Ile Gly Val Ile Pro Thr Glu Gly Ile
    370                 375                 380

Pro Ser Leu Leu Lys Ile Val Leu Pro Pro Asn Phe Gly Gly Leu Pro
385                 390                 395                 400

Ser Leu Tyr Ile Arg Asp Leu Leu Leu Asn Pro Pro Ser Phe Asp Val
                405                 410                 415

Ala Ser Ser Val Gln Glu Ala Cys Arg Leu Met Gly Ser Ile Thr Cys
            420                 425                 430

Ser Ile Pro Glu Phe Thr Cys Ile Pro Ala Ala Lys Leu Val Lys Leu
        435                 440                 445

Leu Glu Ser Lys Glu Val Asn His Ile Glu Phe Cys Arg Ile Lys Asn
    450                 455                 460

Val Leu Asp Glu Val Leu Phe Met Gly Ser Asn Ala Glu Leu Ser Ala
465                 470                 475                 480

Ile Leu Asn Lys Leu Leu Asp Pro Ala Ala Ile Val Thr Gly Phe Lys
                485                 490                 495

Val Glu Ala Asp Ile Leu Val Asn Glu Cys Ser Phe Ile Ser Gln Arg
            500                 505                 510

Ile Ala Glu Val Ile Ser Leu Gly Gly Glu Ser Asp Gln Ala Ile Thr
        515                 520                 525

Ser Ser Glu Tyr Ile Pro Lys Glu Phe Phe Asn Gly Met Glu Ser Ser
    530                 535                 540

Trp Lys Gly Arg Val Lys Arg Val His Ala Glu Glu Glu Phe Ser Asn
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545 550 555 560

Val Asp Ile Ala Ala Glu Ala Leu Ser Thr Ala Val Ile Glu Asp Phe
565 570 575

Leu Pro Ile Ile Ser Arg Val Lys Ser Val Met Ser Ser Asn Gly Ser
580 585 590

Ser Lys Gly Glu Ile Ser Tyr Ala Lys Glu His Glu Ser Val Trp Phe
595 600 605

Lys Gly Arg Arg Phe Thr Pro Asn Val Trp Ala Asn Thr Pro Gly Glu
610 615 620

Leu Gln Ile Lys Gln Leu Lys Pro Ala Ile Asp Ser Lys Gly Arg Lys
625 630 635 640

Val Gly Glu Glu Trp Phe Thr Thr Ile Lys Val Glu Asn Ala Leu Thr
645 650 655

Arg Tyr His Glu Ala Cys Asp Asn Ala Lys Arg Lys Val Leu Glu Leu
660 665 670

Leu Arg Gly Leu Ser Ser Glu Leu Gln Asp Lys Ile Asn Val Leu Val
675 680 685

Phe Cys Ser Thr Met Leu Ile Ile Thr Lys Ala Leu Phe Gly His Val
690 695 700

Ser Glu Gly Arg Arg Arg Gly Trp Val Leu Pro Thr Ile Ser Pro Leu
705 710 715 720

Cys Lys Asp Asn Val Thr Glu Glu Ile Ser Ser Glu Met Glu Leu Ser
725 730 735

Gly Thr Phe Pro Tyr Trp Leu Asp Thr Asn Gln Gly Asn Ala Ile Leu
740 745 750

Asn Asp Val His Met His Ser Leu Phe Ile Leu Thr Gly Pro Asn Gly
755 760 765

Gly Gly Lys Ser Ser Met Leu Arg Ser Val Cys Ala Ala Ala Leu Leu
770 775 780

Gly Ile Cys Gly Leu Met Val Pro Ala Ala Ser Ala Val Ile Pro His
785 790 795 800

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Phe Asp Ser Ile Met Leu His Met Lys Ala Tyr Asp Ser Pro Ala Asp
                805                 810                 815

Gly Lys Ser Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Val
            820                 825                 830

Cys Arg Ala Thr Ala Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg
        835                 840                 845

Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Ile Ile Glu
    850                 855                 860

Arg Leu Asp Asn Val Gly Cys Ile Gly Ile Ile Ser Thr His Leu His
865                 870                 875                 880

Gly Ile Phe Asp Leu Pro Leu Ser Leu His Asn Thr Asp Phe Lys Ala
                885                 890                 895

Met Gly Thr Glu Ile Ile Asp Arg Cys Ile Gln Pro Thr Trp Lys Leu
            900                 905                 910

Met Asp Gly Ile Cys Arg Glu Ser Leu Ala Phe Gln Thr Ala Arg Lys
        915                 920                 925

Glu Gly Met Pro Asp Leu Ile Ile Arg Arg Ala Glu Glu Leu Tyr Leu
    930                 935                 940

Ala Met Ser Thr Asn Ser Lys His Thr Ser Ser Ala Val His His Glu
945                 950                 955                 960

Ile Ser Ile Ala Asn Ser Thr Val Asn Ser Leu Val Glu Lys Pro Asn
                965                 970                 975

Tyr Leu Arg Asn Gly Leu Glu Leu Gln Ser Gly Ser Phe Gly Leu Leu
            980                 985                 990

Arg Lys Glu Ile Glu Ser Val Val  Thr Thr Ile Cys Lys  Lys Lys Leu
        995                 1000                1005

Leu Asp  Leu Tyr Asn Lys Arg  Ser Ile Ser Glu Leu  Ile Glu Val
    1010                1015                1020

Val Cys  Val Ala Val Gly Ala  Arg Glu Gln Pro Pro  Pro Ser Thr
    1025                1030                1035

Val Gly  Arg Ser Ser Ile Tyr  Val Ile Ile Arg Arg  Asp Ser Lys
    1040                1045                1050
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Leu Tyr Ile Gly Gln Thr Asp Asp Leu Val Gly Arg Leu Ser Ala
1055 1060 1065

His Arg Ser Lys Glu Gly Met Gln Asp Ala Thr Ile Leu Tyr Ile
1070 1075 1080

Leu Val Pro Gly Lys Ser Ile Ala Cys Gln Leu Glu Thr Leu Leu
1085 1090 1095

Ile Asn Gln Leu Pro Leu Lys Gly Phe Lys Leu Ile Asn Lys Ala
1100 1105 1110

Asp Gly Lys His Arg Asn Phe Gly Ile Ser Leu Val Pro Gly Glu
1115 1120 1125

Ala Ile Ala Ala
1130

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<213> Sorghum bicolor

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tgccagctgg aaacccttct cataaatcag cttccttcga ggggcttcaa gctcatcaac 120

aaggcagacg gaaagcatag gaacttcggt atatctcgaa tctctggaga ggcaatcgcc 180

acccagctaa actaatcagc taaagatcta atttagttag tcttgacgct agtgagtctc 240

attttgcatc cttcatctct tttgcttttg gctactcaat aggaggcagg aactaactga 300

caccatatgc cgccccaatt ttgtgagatg aattatcagt ggtgctaccc ttgtgcatag 360

taggggccta gggggcgatc ttcccttgtc taagcatgta gtacggtgca aatgattagc 420

aatgcaatga cac 433

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<211> 64
<212> PRT
<213> Sorghum bicolor

<400> 24

Lys Glu Gly Met Gln Asp Ala Thr Ile Leu Tyr Ile Leu Val Pro Gly
1 5 10 15

Lys Ser Val Ala Cys Gln Leu Glu Thr Leu Leu Ile Asn Gln Leu Pro
20 25 30

Ser Arg Gly Phe Lys Leu Ile Asn Lys Ala Asp Gly Lys His Arg Asn
35 40 45

Phe Gly Ile Ser Arg Ile Ser Gly Glu Ala Ile Ala Thr Gln Leu Asn
50 55 60

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agcctacgat agcccagccg atgggaaaag ttcatttcag attgaaatgt cggagatacg 180

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cacagaaact gcaaaaggaa cctgtattgc tggtagcatc atcgaaaggc tggataatgt 300

tggctgccta ggcatcatat caactcacct gcatgggatt tttgacttgc ctctctcact 360

cagcactact gatttcaaag ctatgggaac tgaagtggtc gacgggtgca ttcatccaac 420

atggaaactg atggatggca tctgtagaga aagccttgct tttcaaacag ccaggaggga 480

aggcatgcct gagttcataa tcagaagggc tgaggagcta tatttgacta tgagtacaaa 540

taacaagcag accgcatcaa tggtccacaa tgagcctcgt aatgacagcc ccagtgtaaa 600

tggcttggtt gagaagcctg aatatctgaa atacaggcta gaaattctgc ctggtacctt 660

tgagccg 667

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<211> 222
<212> PRT
<213> Sorghum bicolor

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Ile Cys Gly Leu Met Val Pro Ser Thr Ser Ala Val Ile Pro His Phe
20 25 30

Asp Ser Ile Met Leu His Met Lys Ala Tyr Asp Ser Pro Ala Asp Gly
35 40 45

Lys Ser Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ala Leu Val Ser
50 55 60

Arg Ala Thr Ala Arg Ser Leu Val Leu Ile Gly Glu Ile Cys Arg Gly

65 70 75 80

Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Ile Ile Glu Arg
85 90 95

Leu Asp Asn Val Gly Cys Leu Gly Ile Ile Ser Thr His Leu His Gly
100 105 110

Ile Phe Asp Leu Pro Leu Ser Leu Ser Thr Thr Asp Phe Lys Ala Met
115 120 125

Gly Thr Glu Val Val Asp Gly Cys Ile His Pro Thr Trp Lys Leu Met
130 135 140

Asp Gly Ile Cys Arg Glu Ser Leu Ala Phe Gln Thr Ala Arg Arg Glu
145 150 155 160

Gly Met Pro Glu Phe Ile Ile Arg Arg Ala Glu Glu Leu Tyr Leu Thr
165 170 175

Met Ser Thr Asn Asn Lys Gln Thr Ala Ser Met Val His Asn Glu Pro
180 185 190

Arg Asn Asp Ser Pro Ser Val Asn Gly Leu Val Glu Lys Pro Glu Tyr
195 200 205

Leu Lys Tyr Arg Leu Glu Ile Leu Pro Gly Thr Phe Glu Pro
210 215 220

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<211> 351
<212> DNA
<213> Glycine max

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tcatcaaaga aatagaaaag aatgagaaag tacaaaccac aagaattccg cctcaaggat 180

gtatgcaaaa ataagtaatg atattggcaa gtacgaagct tcgtaacaac tgcttcttct 240

gtcaagcaat cttcagaaga atatgtcttc atggtctcta gtaccatatt aatgcaataa 300

cccctcgcag aatgagatat tcctactaca ggcattggtt ctgcctcgtg c 351

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agtaagattg gtgaaatagt atctctggat gatgagaatg atcagaaaat caactcgttc 180

tcttttattc ctcacgaatt ttttgaggat atggagtcta aatggaaagg tcgaataaaa 240

agaatccaca tagatgatgt attcactgca gtggaaaaag cagctgaggc cttacatata 300

gcagtcactg aagattttgt tcctgtagtt gctagaataa aggctattgt agcccctctc 360

ggaggtccta acggagaaat atcttatgct cgggagcaag aagcag 406

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<212> DNA
<213> Glycine max

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cactacactc cttctctatt tcccattttc acttcattcg ctccctctcg tttccttaga 120

ataaatggat gtgtaaagaa tgtgtcgagt tatacggata agaaggtttc aaggggagt 180

agtagggcca ccaagaagcc caaaatacca aataacgttt tagatgataa agaccttcct 240

cacatactgt ggtggaagga gaggttgcaa atgtgcagaa agttttcaac tgtccagtta 300

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Cys Ser Leu Ala His Tyr Thr Pro Ser Leu Phe Pro Ile Phe Thr Ser
            20                  25                  30

ttc gct ccc tct cgt ttc ctt aga ata aat gga tgt gta aag aat gtg      144
Phe Ala Pro Ser Arg Phe Leu Arg Ile Asn Gly Cys Val Lys Asn Val
        35                  40                  45

tcg agt tat acg gat aag aag gtt tca agg ggg agt agt agg gcc acc      192
Ser Ser Tyr Thr Asp Lys Lys Val Ser Arg Gly Ser Ser Arg Ala Thr
    50                  55                  60

aag aag ccc aaa ata cca aat aac gtt tta gat gat aaa gac ctt cct      240
Lys Lys Pro Lys Ile Pro Asn Asn Val Leu Asp Asp Lys Asp Leu Pro
65                  70                  75                  80

cac ata ctg tgg tgg aag gag agg ttg caa atg tgc aga aag ttt tca      288
His Ile Leu Trp Trp Lys Glu Arg Leu Gln Met Cys Arg Lys Phe Ser
                85                  90                  95

act gtc cag tta att gaa aga ctt gaa ttt tct aat ttg ctt ggc ctg      336
Thr Val Gln Leu Ile Glu Arg Leu Glu Phe Ser Asn Leu Leu Gly Leu
            100                 105                 110

aat tcc aac ttg aaa aat gga agt ctg aag gaa gga aca ctc aac tgg      384
Asn Ser Asn Leu Lys Asn Gly Ser Leu Lys Glu Gly Thr Leu Asn Trp
        115                 120                 125

gaa atg ttg caa ttc aag tca aaa ttt cca cgt caa gta ttg ctt tgc      432
Glu Met Leu Gln Phe Lys Ser Lys Phe Pro Arg Gln Val Leu Leu Cys
    130                 135                 140
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aga gtt ggg gaa ttc tat gaa gct tgg gga ata gat gct tgt att ctt      480
Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Ile Leu
145                 150                 155                 160

gtt gaa tat gtg ggt tta aat ccc att ggt ggt ctg cga tca gat agt      528
Val Glu Tyr Val Gly Leu Asn Pro Ile Gly Gly Leu Arg Ser Asp Ser
                165                 170                 175

atc cca aga gct agt tgt cct gtc gtg aat ctt cgg cag act tta gat      576
Ile Pro Arg Ala Ser Cys Pro Val Val Asn Leu Arg Gln Thr Leu Asp
            180                 185                 190

gat ctg aca aca aat ggt tat tca gtg tgc att gtg gag gag gct cag      624
Asp Leu Thr Thr Asn Gly Tyr Ser Val Cys Ile Val Glu Glu Ala Gln
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ggc cca agt caa gct cga tcc agg aaa cgt cgc ttt ata tct ggg cat      672
Gly Pro Ser Gln Ala Arg Ser Arg Lys Arg Arg Phe Ile Ser Gly His
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gct cat cct gga aat ccc tat gta tat gga ctt gct aca gtt gat cat      720
Ala His Pro Gly Asn Pro Tyr Val Tyr Gly Leu Ala Thr Val Asp His
225                 230                 235                 240

gat ctt aac ttt cca gaa cca atg cct gta gta gga ata tct cat tct      768
Asp Leu Asn Phe Pro Glu Pro Met Pro Val Val Gly Ile Ser His Ser
                245                 250                 255

gcg agg ggt tat tgc att aat atg gta cta gag acc atg aag aca tat      816
Ala Arg Gly Tyr Cys Ile Asn Met Val Leu Glu Thr Met Lys Thr Tyr
            260                 265                 270

tct tct gaa gat tgc ttg aca gaa gaa gca gtt gtt acg aag ctt cgt      864
Ser Ser Glu Asp Cys Leu Thr Glu Glu Ala Val Val Thr Lys Leu Arg
        275                 280                 285

act tgc caa tat cat tac tta ttt ttg cat aca tcc ttg agg cgg aat      912
Thr Cys Gln Tyr His Tyr Leu Phe Leu His Thr Ser Leu Arg Arg Asn
    290                 295                 300

tct tgt gga acc tgc aac tgg gga gaa ttt ggt gag gga ggg cta tta      960
Ser Cys Gly Thr Cys Asn Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu
305                 310                 315                 320

tgg gga gaa tgt agt tct aga cat ttt gat tgg ttt gat ggc aac cct     1008
Trp Gly Glu Cys Ser Ser Arg His Phe Asp Trp Phe Asp Gly Asn Pro
                325                 330                 335

gtc tcc gat ctt ttg gcc aag gta aag gaa ctt tat agt att gat gat     1056
Val Ser Asp Leu Leu Ala Lys Val Lys Glu Leu Tyr Ser Ile Asp Asp
            340                 345                 350

gag gtt acc ttt cgg aac aca act gtg tct tca gga cat agg gct cga     1104
Glu Val Thr Phe Arg Asn Thr Thr Val Ser Ser Gly His Arg Ala Arg
        355                 360                 365

cca tta act ctt gga aca tct act caa att ggt gcc att cca aca gaa     1152
Pro Leu Thr Leu Gly Thr Ser Thr Gln Ile Gly Ala Ile Pro Thr Glu
    370                 375                 380

gga ata cct tct ttg ttg aag gtt tta ctt cca tca aat tgc aat gga     1200
Gly Ile Pro Ser Leu Leu Lys Val Leu Leu Pro Ser Asn Cys Asn Gly
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tta cca gta ttg tac ata agg gaa ctt ctt ttg aat cct cct tca tat     1248
Leu Pro Val Leu Tyr Ile Arg Glu Leu Leu Leu Asn Pro Pro Ser Tyr
                405                 410                 415

gag att gca tcc aaa att caa gca aca tgc aaa ctt atg agc agt gta     1296
Glu Ile Ala Ser Lys Ile Gln Ala Thr Cys Lys Leu Met Ser Ser Val
            420                 425                 430

acg tgt tca att cca gaa ttt aca tgt gtt tcg tca gca aag ctt gta     1344
Thr Cys Ser Ile Pro Glu Phe Thr Cys Val Ser Ser Ala Lys Leu Val
        435                 440                 445

aag cta ctt gaa tgg agg gag gtc aat cat atg gaa ttt tgt aga ata     1392
Lys Leu Leu Glu Trp Arg Glu Val Asn His Met Glu Phe Cys Arg Ile
    450                 455                 460

aag aat gta ctg gat gaa att ttg cag atg tat agt acc tct gag ctc     1440
Lys Asn Val Leu Asp Glu Ile Leu Gln Met Tyr Ser Thr Ser Glu Leu
465                 470                 475                 480

aat gaa ata ttg aaa cat tta atc gag ccc aca tgg gtg gca act ggg     1488
Asn Glu Ile Leu Lys His Leu Ile Glu Pro Thr Trp Val Ala Thr Gly
                485                 490                 495

tta gaa att gac ttt gaa acc ttg gtt gca gga tgt gag atc gca tct     1536
Leu Glu Ile Asp Phe Glu Thr Leu Val Ala Gly Cys Glu Ile Ala Ser
            500                 505                 510

agt aag att ggt gaa ata gta tct ctg gat gat gag aat gat cag aaa     1584
Ser Lys Ile Gly Glu Ile Val Ser Leu Asp Asp Glu Asn Asp Gln Lys
        515                 520                 525

atc aac tcg ttc tct ttt att cct cac gaa ttt ttt gag gat atg gag     1632
Ile Asn Ser Phe Ser Phe Ile Pro His Glu Phe Phe Glu Asp Met Glu
    530                 535                 540

tct aaa tgg aaa ggt cga ata aaa aga atc cac ata gat gat gta ttc     1680
Ser Lys Trp Lys Gly Arg Ile Lys Arg Ile His Ile Asp Asp Val Phe
545                 550                 555                 560

act gca gtg gaa aaa gca gct gag gcc tta cat ata gca gtc act gaa     1728
Thr Ala Val Glu Lys Ala Ala Glu Ala Leu His Ile Ala Val Thr Glu
                565                 570                 575

gat ttt gtt cct gtt gtt tct aga ata aag gct att gta gcc cct ctc     1776
Asp Phe Val Pro Val Val Ser Arg Ile Lys Ala Ile Val Ala Pro Leu
            580                 585                 590

gga ggt cct aag gga gaa ata tct tat gct cgg gag caa gaa gca gtt     1824
Gly Gly Pro Lys Gly Glu Ile Ser Tyr Ala Arg Glu Gln Glu Ala Val
        595                 600                 605

tgg ttc aaa ggc aaa cgc ttt aca ccg aat ttg tgg gct ggt agc cct     1872
Trp Phe Lys Gly Lys Arg Phe Thr Pro Asn Leu Trp Ala Gly Ser Pro
    610                 615                 620

gga gag gaa caa att aaa cag ctt agg cat gct tta gat tct aaa ggt     1920
Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys Gly
625                 630                 635                 640

aga aag gta ggg gag gaa tgg ttt acc aca cca aag gtc gag gct gca     1968
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Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ala Ala
                645                 650                 655

tta aca agg tac cat gaa gca aat gcc aag gca aaa gaa aga gtt ttg     2016
Leu Thr Arg Tyr His Glu Ala Asn Ala Lys Ala Lys Glu Arg Val Leu
            660                 665                 670

gaa att tta agg gga ctc gct gct gag ttg caa tac agt ata aac att     2064
Glu Ile Leu Arg Gly Leu Ala Ala Glu Leu Gln Tyr Ser Ile Asn Ile
        675                 680                 685

ctt gtc ttt tct tcc atg ttg ctt gtt att gcc aaa gct tta ttt gct     2112
Leu Val Phe Ser Ser Met Leu Leu Val Ile Ala Lys Ala Leu Phe Ala
    690                 695                 700

cat gca agt gaa ggg aga aga agg aga tgg gtc ttt ccc acg ctt gta     2160
His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu Val
705                 710                 715                 720

gaa tcc cat ggg ttt gag gat gtg aag tca ttg gac aaa acc cat ggg     2208
Glu Ser His Gly Phe Glu Asp Val Lys Ser Leu Asp Lys Thr His Gly
                725                 730                 735

atg aag ata agt ggt tta ttg cca tat tgg ttc cac ata gca gaa ggt     2256
Met Lys Ile Ser Gly Leu Leu Pro Tyr Trp Phe His Ile Ala Glu Gly
            740                 745                 750

gtt gtg cgt aat gat gtt gat atg caa tca tta ttt ctg ttg aca gga     2304
Val Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr Gly
        755                 760                 765

ccg aat ggt ggt ggg aaa tca agt ttt ctt agg tca att tgt gct gct     2352
Pro Asn Gly Gly Gly Lys Ser Ser Phe Leu Arg Ser Ile Cys Ala Ala
    770                 775                 780

gca cta ctt ggg ata tgt gga ctc atg gtt cct gca gaa tca gcc cta     2400
Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala Leu
785                 790                 795                 800

att cct tat ttt gac tcc atc acg ctt cat atg aag tca tat gat agt     2448
Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp Ser
                805                 810                 815

cca gct gat aaa aag agt tcc ttt cag gtt gaa atg tca gaa ctt cga     2496
Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu Arg
            820                 825                 830

tcc atc att ggc gga aca acc aac agg agc ctt gta ctt gtt gat gaa     2544
Ser Ile Ile Gly Gly Thr Thr Asn Arg Ser Leu Val Leu Val Asp Glu
        835                 840                 845

ata tgc cga gga aca gaa act gca aaa ggg act tgc att gct ggt agc     2592
Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser
    850                 855                 860

atc att gaa acc ctt gat gga att ggg tgt ctg ggt att gta tcc act     2640
Ile Ile Glu Thr Leu Asp Gly Ile Gly Cys Leu Gly Ile Val Ser Thr
865                 870                 875                 880

cac ttg cat gga ata ttt act ttg ccc cta aac aaa aaa aac act gtg     2688
His Leu His Gly Ile Phe Thr Leu Pro Leu Asn Lys Lys Asn Thr Val
                885                 890                 895
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cac aaa gca atg ggc aca aca tcc att gat gga caa ata atg cct aca     2736
His Lys Ala Met Gly Thr Thr Ser Ile Asp Gly Gln Ile Met Pro Thr
            900                 905                 910

tgg aag ttg aca gat gga gtt tgt aaa gaa agt ctt gct ttt gaa acg     2784
Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu Thr
        915                 920                 925

gct aag agg gaa gga att cct gag cat att gtt aga aga gct gaa tat     2832
Ala Lys Arg Glu Gly Ile Pro Glu His Ile Val Arg Arg Ala Glu Tyr
    930                 935                 940

ctt tat cag ttg gtt tat gct aag gaa atg ctt ttt gca gaa aat ttc     2880
Leu Tyr Gln Leu Val Tyr Ala Lys Glu Met Leu Phe Ala Glu Asn Phe
945                 950                 955                 960

cca aat gaa gaa aag ttt tct acc tgc atc aat gtt aat aat ttg aat     2928
Pro Asn Glu Glu Lys Phe Ser Thr Cys Ile Asn Val Asn Asn Leu Asn
                965                 970                 975

gga aca cat ctt cat tca aaa agg ttc cta tca gga gct aat caa atg     2976
Gly Thr His Leu His Ser Lys Arg Phe Leu Ser Gly Ala Asn Gln Met
            980                 985                 990

gaa gtt tta cgc gag gaa gtt gag  aga gct gtc act gtg  att tgc cag   3024
Glu Val Leu Arg Glu Glu Val Glu  Arg Ala Val Thr Val  Ile Cys Gln
        995                 1000                1005

gat cat  ata aag gac cta aaa  tgc aaa aag att gca  ttg gag ctt      3069
Asp His  Ile Lys Asp Leu Lys  Cys Lys Lys Ile Ala  Leu Glu Leu
    1010                1015                1020

act gag  ata aaa tgt ctc ata  att ggt aca agg gag  cta cca cct      3114
Thr Glu  Ile Lys Cys Leu Ile  Ile Gly Thr Arg Glu  Leu Pro Pro
    1025                1030                1035

cca tcg  gtt gta ggt tct tca  agc gtc tat gtg atg  ttc aga cca      3159
Pro Ser  Val Val Gly Ser Ser  Ser Val Tyr Val Met  Phe Arg Pro
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gat aag  aaa ctc tat gta gga  gag act gat gat ctc  gag gga cgg      3204
Asp Lys  Lys Leu Tyr Val Gly  Glu Thr Asp Asp Leu  Glu Gly Arg
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gtc cga  aga cat cga tta aag  gaa gga atg cat gat  gca tca ttc      3249
Val Arg  Arg His Arg Leu Lys  Glu Gly Met His Asp  Ala Ser Phe
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ctt tat  ttt ctt gtc cca ggt  aaa agc ttg gca tgc  caa ttt gaa      3294
Leu Tyr  Phe Leu Val Pro Gly  Lys Ser Leu Ala Cys  Gln Phe Glu
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tct ctg  ctc atc aac caa ctt  tct ggt caa ggc ttc  caa ctg agc      3339
Ser Leu  Leu Ile Asn Gln Leu  Ser Gly Gln Gly Phe  Gln Leu Ser
    1100                1105                1110

aat ata  gct gat ggt aaa cat  agg aat ttt ggc act  tcc aac ctg      3384
Asn Ile  Ala Asp Gly Lys His  Arg Asn Phe Gly Thr  Ser Asn Leu
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Tyr Thr
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Phe Ala Pro Ser Arg Phe Leu Arg Ile Asn Gly Cys Val Lys Asn Val
        35                  40                  45

Ser Ser Tyr Thr Asp Lys Lys Val Ser Arg Gly Ser Ser Arg Ala Thr
    50                  55                  60

Lys Lys Pro Lys Ile Pro Asn Asn Val Leu Asp Asp Lys Asp Leu Pro
65                  70                  75                  80

His Ile Leu Trp Trp Lys Glu Arg Leu Gln Met Cys Arg Lys Phe Ser
                85                  90                  95

Thr Val Gln Leu Ile Glu Arg Leu Glu Phe Ser Asn Leu Leu Gly Leu
            100                 105                 110

Asn Ser Asn Leu Lys Asn Gly Ser Leu Lys Glu Gly Thr Leu Asn Trp
        115                 120                 125

Glu Met Leu Gln Phe Lys Ser Lys Phe Pro Arg Gln Val Leu Leu Cys
    130                 135                 140

Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Ile Leu
145                 150                 155                 160

Val Glu Tyr Val Gly Leu Asn Pro Ile Gly Gly Leu Arg Ser Asp Ser
                165                 170                 175

Ile Pro Arg Ala Ser Cys Pro Val Val Asn Leu Arg Gln Thr Leu Asp
            180                 185                 190

Asp Leu Thr Thr Asn Gly Tyr Ser Val Cys Ile Val Glu Glu Ala Gln
        195                 200                 205

Gly Pro Ser Gln Ala Arg Ser Arg Lys Arg Arg Phe Ile Ser Gly His
    210                 215                 220
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Ala His Pro Gly Asn Pro Tyr Val Tyr Gly Leu Ala Thr Val Asp His
225                 230                 235                 240

Asp Leu Asn Phe Pro Glu Pro Met Pro Val Val Gly Ile Ser His Ser
                245                 250                 255

Ala Arg Gly Tyr Cys Ile Asn Met Val Leu Glu Thr Met Lys Thr Tyr
            260                 265                 270

Ser Ser Glu Asp Cys Leu Thr Glu Glu Ala Val Val Thr Lys Leu Arg
        275                 280                 285

Thr Cys Gln Tyr His Tyr Leu Phe Leu His Thr Ser Leu Arg Arg Asn
    290                 295                 300

Ser Cys Gly Thr Cys Asn Trp Gly Glu Phe Gly Glu Gly Gly Leu Leu
305                 310                 315                 320

Trp Gly Glu Cys Ser Ser Arg His Phe Asp Trp Phe Asp Gly Asn Pro
                325                 330                 335

Val Ser Asp Leu Leu Ala Lys Val Lys Glu Leu Tyr Ser Ile Asp Asp
            340                 345                 350

Glu Val Thr Phe Arg Asn Thr Thr Val Ser Ser Gly His Arg Ala Arg
        355                 360                 365

Pro Leu Thr Leu Gly Thr Ser Thr Gln Ile Gly Ala Ile Pro Thr Glu
    370                 375                 380

Gly Ile Pro Ser Leu Leu Lys Val Leu Leu Pro Ser Asn Cys Asn Gly
385                 390                 395                 400

Leu Pro Val Leu Tyr Ile Arg Glu Leu Leu Leu Asn Pro Pro Ser Tyr
                405                 410                 415

Glu Ile Ala Ser Lys Ile Gln Ala Thr Cys Lys Leu Met Ser Ser Val
            420                 425                 430

Thr Cys Ser Ile Pro Glu Phe Thr Cys Val Ser Ser Ala Lys Leu Val
        435                 440                 445

Lys Leu Leu Glu Trp Arg Glu Val Asn His Met Glu Phe Cys Arg Ile
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Lys Asn Val Leu Asp Glu Ile Leu Gln Met Tyr Ser Thr Ser Glu Leu
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Leu Glu Ile Asp Phe Glu Thr Leu Val Ala Gly Cys Glu Ile Ala Ser
            500                 505                 510

Ser Lys Ile Gly Glu Ile Val Ser Leu Asp Asp Glu Asn Asp Gln Lys
        515                 520                 525

Ile Asn Ser Phe Ser Phe Ile Pro His Glu Phe Phe Glu Asp Met Glu
    530                 535                 540

Ser Lys Trp Lys Gly Arg Ile Lys Arg Ile His Ile Asp Asp Val Phe
545                 550                 555                 560

Thr Ala Val Glu Lys Ala Ala Glu Ala Leu His Ile Ala Val Thr Glu
                565                 570                 575

Asp Phe Val Pro Val Val Ser Arg Ile Lys Ala Ile Val Ala Pro Leu
            580                 585                 590

Gly Gly Pro Lys Gly Glu Ile Ser Tyr Ala Arg Glu Gln Glu Ala Val
        595                 600                 605

Trp Phe Lys Gly Lys Arg Phe Thr Pro Asn Leu Trp Ala Gly Ser Pro
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Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys Gly
625                 630                 635                 640

Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ala Ala
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Leu Thr Arg Tyr His Glu Ala Asn Ala Lys Ala Lys Glu Arg Val Leu
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Glu Ile Leu Arg Gly Leu Ala Ala Glu Leu Gln Tyr Ser Ile Asn Ile
        675                 680                 685

Leu Val Phe Ser Ser Met Leu Leu Val Ile Ala Lys Ala Leu Phe Ala
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His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu Val
705                 710                 715                 720
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Glu Ser His Gly Phe Glu Asp Val Lys Ser Leu Asp Lys Thr His Gly
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Met Lys Ile Ser Gly Leu Leu Pro Tyr Trp Phe His Ile Ala Glu Gly
            740                 745                 750

Val Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr Gly
        755                 760                 765

Pro Asn Gly Gly Gly Lys Ser Ser Phe Leu Arg Ser Ile Cys Ala Ala
    770                 775                 780

Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala Leu
785                 790                 795                 800

Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp Ser
                805                 810                 815

Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu Arg
            820                 825                 830

Ser Ile Ile Gly Gly Thr Thr Asn Arg Ser Leu Val Leu Val Asp Glu
        835                 840                 845

Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser
    850                 855                 860

Ile Ile Glu Thr Leu Asp Gly Ile Gly Cys Leu Gly Ile Val Ser Thr
865                 870                 875                 880

His Leu His Gly Ile Phe Thr Leu Pro Leu Asn Lys Lys Asn Thr Val
                885                 890                 895

His Lys Ala Met Gly Thr Thr Ser Ile Asp Gly Gln Ile Met Pro Thr
            900                 905                 910

Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu Thr
        915                 920                 925

Ala Lys Arg Glu Gly Ile Pro Glu His Ile Val Arg Arg Ala Glu Tyr
    930                 935                 940

Leu Tyr Gln Leu Val Tyr Ala Lys Glu Met Leu Phe Ala Glu Asn Phe
945                 950                 955                 960

Pro Asn Glu Glu Lys Phe Ser Thr Cys Ile Asn Val Asn Asn Leu Asn
                965                 970                 975
```

```
Gly Thr His Leu His Ser Lys Arg Phe Leu Ser Gly Ala Asn Gln Met
            980                 985                 990

Glu Val Leu Arg Glu Glu Val Glu  Arg Ala Val Thr Val  Ile Cys Gln
        995                 1000                1005

Asp His  Ile Lys Asp Leu Lys  Cys Lys Lys Ile Ala  Leu Glu Leu
    1010                1015                1020

Thr Glu  Ile Lys Cys Leu Ile  Ile Gly Thr Arg Glu  Leu Pro Pro
    1025                1030                1035

Pro Ser  Val Val Gly Ser Ser  Ser Val Tyr Val Met  Phe Arg Pro
    1040                1045                1050

Asp Lys  Lys Leu Tyr Val Gly  Glu Thr Asp Asp Leu  Glu Gly Arg
    1055                1060                1065

Val Arg  Arg His Arg Leu Lys  Glu Gly Met His Asp  Ala Ser Phe
    1070                1075                1080

Leu Tyr  Phe Leu Val Pro Gly  Lys Ser Leu Ala Cys  Gln Phe Glu
    1085                1090                1095

Ser Leu  Leu Ile Asn Gln Leu  Ser Gly Gln Gly Phe  Gln Leu Ser
    1100                1105                1110

Asn Ile  Ala Asp Gly Lys His  Arg Asn Phe Gly Thr  Ser Asn Leu
    1115                1120                1125

Tyr Thr
    1130
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<210> 32
<211> 757
<212> DNA
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (512)..(512)
<223> n is a, c, g, or t

<400> 32

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ccgcctctct cgccccccac ttcccacgcc ccacgccgcc tcccattcca gttccagcgt     60

ggacgcgacg ccggcgcgga gacgcggcgt ctcgaagcac tagccccctg ttgttcttcc    120

gcgccggcgc gccggcgcca tgcaccgggt gctcgtgagc tcgctcgtgg ccgccacgcc    180
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gcggtggctc cccctcgccg actccatcct ccggcgccgc cgcccgcgct gctcccctct 240

tcccatgctg ctattcgacc ggaggacttg gtccaagcca aggaaggtct cacgaggcat 300

ttcagtggca tctaggaaag ctaacaaaca gggagaatat tgtgatgaaa gcatgctatc 360

tcatatcatg tggtggaaag agaaaatgga gaagtgcaga aaaccatcat ctgtacagtt 420

gactcagagg cttgtgtatt cgaatatatt agggttggat ccgaatttaa gaaatggaag 480

cttgaaagat ggaaccctga acatggagat tntgctattt aaatcaaaat ttcctcgtga 540

ggttctactt tgcagaaaca tgcaggctta aattctcttt ggagggttgc gttctgacag 600

aattcctaaa gctgggtgtc cagccggaat ttacggagac attggatgag ttgactcgat 660

gtgggaattc tgtgtgcaaa gtgaagaaat tacaggccga cccaagccct gccccggaaa 720

gtcgattaat tctgggcatg cccatcctgg agcccta 757

<210> 33
<211> 139
<212> PRT
<213> Saccharum officinarum

<220>
<221> misc_feature
<222> (125)..(125)
<223> Xaa can be any naturally occurring amino acid

<400> 33

Met His Arg Val Leu Val Ser Ser Leu Val Ala Ala Thr Pro Arg Trp
1 5 10 15

Leu Pro Leu Ala Asp Ser Ile Leu Arg Arg Arg Arg Pro Arg Cys Ser
20 25 30

Pro Leu Pro Met Leu Leu Phe Asp Arg Arg Thr Trp Ser Lys Pro Arg
35 40 45

Lys Val Ser Arg Gly Ile Ser Val Ala Ser Arg Lys Ala Asn Lys Gln
50 55 60

Gly Glu Tyr Cys Asp Glu Ser Met Leu Ser His Ile Met Trp Trp Lys
65 70 75 80

Glu Lys Met Glu Lys Cys Arg Lys Pro Ser Ser Val Gln Leu Thr Gln
85 90 95

Arg Leu Val Tyr Ser Asn Ile Leu Gly Leu Asp Pro Asn Leu Arg Asn
100 105 110

Gly Ser Leu Lys Asp Gly Thr Leu Asn Met Glu Ile Xaa Leu Phe Lys

115 120 125

Ser Lys Phe Pro Arg Glu Val Leu Leu Cys Arg
130 135

<210> 34
<211> 504
<212> DNA
<213> Saccharum officinarum

<400> 34
cacgtacctg tcctgaattc cccgaccgac ccatgcgtga gaacaagctt taattaaaac 60

atacctaagt atcttctggg gtcgccttca cgcccacaga ggggaggaag gcatgcaaga 120

tgctaccacc ctatacatct tggttcctgg caagagcgtt gcctgccagc tagaaaccct 180

tctcataaat cagcttcctt ctgagggctt caagctcatc aacaaggtag acggaaagca 240

taggaacttc ggtatatttc gaatctctgg agaggcaatt gctactcaac taaactaatc 300

acgtgaagat ctaatttagc tagacgacac tagtgagtct cattttggct actcaatagg 360

aggcaggagc taactgacac catgccgccc caatattgtt gaactgatag cggagctagc 420

cttgaccata atacgggcat ctttttctcg tctaatgatg tagtacaatg caaatgatta 480

gcaatgcaat gacactcgtt gtgc 504

<210> 35
<211> 72
<212> PRT
<213> Saccharum officinarum

<400> 35

Gly Arg Leu His Ala His Arg Gly Glu Glu Gly Met Gln Asp Ala Thr
1 5 10 15

Thr Leu Tyr Ile Leu Val Pro Gly Lys Ser Val Ala Cys Gln Leu Glu
20 25 30

Thr Leu Leu Ile Asn Gln Leu Pro Ser Glu Gly Phe Lys Leu Ile Asn
35 40 45

Lys Val Asp Gly Lys His Arg Asn Phe Gly Ile Phe Arg Ile Ser Gly
50 55 60

Glu Ala Ile Ala Thr Gln Leu Asn
65 70

<210> 36
<211> 671
<212> DNA
<213> Nicotiana tabacum

<400> 36
aacaattctt agccttctat gcttcagttt gtaaatgcta ctgttgagat tttttgttgt 60

ctatttacag ctggtcaagt tgcttgagtt gagggaggca aatcatgtag agttctgcaa 120

aataaagaat gtggtcgatg aaatactgca gatgtacaga aattcagagc ttcgtgctat 180

tttagagtca gctgatggat cctacttggg tggcaaccgg gttaaaagtc gattttgata 240

ctctagtgaa tgaatgtggg gagatttctg gtagaatcag tgaaataata tctgtacatg 300

gtgaaagtga tcaaaagata agtccctatc ctatcatccc aaatgatttt tttgaagata 360

tggagtcgcc atggaaaggt cgtgtcaaga ggatccattt ggaggaagca tatgcagaag 420

tagacaaggc tgcagatgct ttatctttgg ctgtgagtct ctttttattt atcttcaaca 480

atcctaatga tttacaagtt gtgcatctgt gtgcgcttta atactctttc attagctaag 540

atatacattt gctgtaaagg cagtcagctt ttcaacgtcc agtaaaagct ttttgataaa 600

tccagtaata ttatctagga atttactgat cgatgaacaa ttttggggta atcgatagac 660

aaataaacaa g 671

<210> 37
<211> 488
<212> DNA
<213> Lycopersicon esculentum

<400> 37
gtttggtgaa ggtggacttt tgtggggaga atgtaatgct agacagcagg aatggttgga 60

tggcaatcct atcgatgagc ttttgttcaa ggtaaaagag ctttatggtc tcaatgatga 120

cattccattc agaaatgtca ctgttgtttc agaaaatagg ccccgtcctt tacaccttgg 180

aactgccaca caaattggtg ctattccaac cgaagggatt ccatgtttgt taaaggtgtt 240

gcttcctcct cattgcagtg gtctaccagt cctgtatatt agggatcttc ttttaaatcc 300

accaccctat gagatttctt cagacattca agaggcatgc agacttatga tgagtgtcac 360

atgttcaatt cctgatttta cctgtatttc atctgcaaag ctggtcaagc tgcttgagtt 420

gagggaggca aatcacgttg agttctgcaa aataaagagc atggtcgaag agatactgca 480

gttgtata 488

<210> 38
<211> 3373
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> misc_feature
<222> (689)..(689)
<223> n is a, c, g, or t

<400> 38
atgtattggg ttacggcaaa aaacgtcgtc gtttcagttc cccgttggcg ttcactgtcc 60
cttttcctcc gtccaccact tcgccggcgt ttcttatctt tctctccaca tactctgtgc 120
cgagagcaga tacgttgcgt gaaggagcgg aagtttttg ccacaacggc aaaaaaactc 180
aaacaaccaa aaagtattcc agaggaaaaa gactatgtta atattatgtg gtggaaagag 240
agaatggaat tcttgagaaa gccttcttcc gctcttctgg ctaagaggct tacatattgt 300
aacttgctgg gtgtggatcc gagtttgaga aatggaagtc ttaaagaggg aacacttaac 360
tcggagatgt tgcagttcaa gtcaaaattt ccacgtgaag ttttgctctg tagagtaggt 420
gatttttatg aagctattgg attcgatgct tgtattcttg tggaatatgc tggtttaaat 480
ccatttggtg gcctgcactc agatagtata ccaaaagctg gttgtccagt tgtgaatcta 540
agacagacgc ttgatgatct cacacgtaat ggtttctctg tgtgcgtcgt ggaggaagtt 600
cagggtccaa ctcaagctcg tgctcgtaag agtcgattta tatcagggca tgcacatcca 660
ggcagtccct atgtttttgg ccttgttgna gatgatcaag atcttgattt tccagaacca 720
atgcctgttg ttggaatatc ccgttcagcg aaggggtatt gcattatctc tgtttacgag 780
actatgaaga cttactctgt ggaagatggc ctaactgaag aagccgtagt caccaaactt 840
cgtacttgtc gatgccatca ttttttttg cataattcat tgaagaacaa ttcctcagga 900
acatcgcgtt ggggagagtt tggtgaaggt ggacttttgt ggggagaatg taatgctaga 960
cagcaggaat ggttggatgg caatcctatc gatgagcttt tgttcaaggt aaaagagctt 1020
tatggtctca atgatgacat tccattcaga aatgtcactg ttgtttcaga aaataggccc 1080
cgtcctttac accttggaac tgccacacaa attggtgcta ttccaaccga agggattcca 1140
tgtttgttaa aggtgttgct tcctcctcat tgcagtggtc taccagtcct gtatattagg 1200
gatcttcttt taaatccacc agcctatgag atttcttcag acatacaaga ggcatgcaga 1260
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gtcgaagaga tactgcagtt gtatagaaat tcagagcttc gtgctatwgt agagttactg 1440
atggatccta cttgggtggc aactgggttg aaagttgatt ttgatacact agtaaatgaa 1500
tgtggaaaga tttcttgtag aatcagtgaa ataatatccg tacatggtga aaatgatcaa 1560
aagattagtt cctatcctat catcccaaat gatttctttg aagatatgga gttgttgtgg 1620
aaaggccgtg tcaagaggat ccatttggag gaagcatatg cagaagtaga aaaggctgcg 1680
gatgctttat ctttagccat aacagaagat ttcctaccta ttatttcaag aataagggcc 1740
acgatggccc cacttggagg aactaaaggg gagattttgt atgcccgtga gcatggagct 1800
gtatggttta agggaaagag atttgtacca actgtttggg ctggaaccgc tggagaagaa 1860

caaattaagc aactcagacc tgctctagat tcaaagggga agaaggttgg agaagaatgg 1920

ttcactacaa tgagggtgga agatgcaata gctaggtatc acgaggcaag tgctagggca 1980

aagtcaaggg tcttggaatt gctaagggga ctttcttctg aattactatc taagatcaat 2040

atccttatct ttgcatctgt cttgaatgtg atagcaaaat cattattttc tcatgtgagt 2100

gaaggaagaa gaagaaattg gattttccca acaatcacac aatttaacaa atgtcaggac 2160

acagaggcac ttaatggaac tgatggaatg aagataattg gtctatctcc ttattggttt 2220

gatgcagcac gagggactgg tgtacaggat acagtagata tgcagtccat gtttctttta 2280

acaggtccaa atggtggggg caaatcaagc ttgctgcgtt cgttgtgtgc agctgcattg 2340

ctaggaatgt gtgggttcat ggttccagct gaatcagctg tcattcctca ttttgactca 2400

attatgctgc atatgaaatc atatgatagt cctgttgatg gaaaaagttc atttcagatt 2460

gaaatgtctg aaattcggtc tctgattact ggtgccactt caagaagtct tgtacttata 2520

gatgaaatat gtcgaggaac agaaacagca aaagggacat gtattgctgg aagtgtcata 2580

gaaaccctgg acgaaattgg ctgtttggga attgtatcaa cccacttgca tggaatattt 2640

gatttacccc tgaaaatcaa gaagaccgtg tataaagcaa tgggagctga atatgttgac 2700

ggtcaaccaa taccaacttg gaaactcatt gatgggatct gtaaagagag tctagcattt 2760

gaaacagctc agagagaagg aattccagaa atattaatcc aaagagcaga agaattgtat 2820

aattcagctt acgggaatca gataccaagg aagatagacc aaataagacc tcttcgttca 2880

gatattgacc tcaatagcac agataacagt tctgaccaat taaatggtac aagacaaata 2940

gctttggatt ctagcacaaa gttaatgcat cgaatgggaa tttcaagcaa gaaacttgaa 3000

gatgctatct gtcttatctg tgagaagaag ttaattgagc tgtataaaat gaaaaatccg 3060

tcagaaatgc caatggtgaa ttgcgttctt attgctgcca gggaacagcc ggctccatca 3120

acaattggtg cttcaagtgt ctatataatg ctaagacctg acaaaaagtt gtatgttgga 3180

cagactgatg atcttgaggg cagagtacgt gctcatcgct tgaaggaggg aatggaaaac 3240

gcgtcattcc tatatttctt agtctctggc aagagcatcg cctgccaatt ggaaactctt 3300

ctaataaatc aacttcctaa tcatggtttt cagctaacaa acgttgctga tggtaagcat 3360

cgtaattttg gca 3373

<210> 39
<211> 3373
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> CDS
<222> (1)..(3372)

<220>
<221> misc_feature
<222> (689)..(689)
<223> n is a, c, g, or t

<400> 39

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atg tat tgg gtt acg gca aaa aac gtc gtc gtt tca gtt ccc cgt tgg       48
Met Tyr Trp Val Thr Ala Lys Asn Val Val Val Ser Val Pro Arg Trp
1               5                  10                  15

cgt tca ctg tcc ctt ttc ctc cgt cca cca ctt cgc cgg cgt ttc tta       96
Arg Ser Leu Ser Leu Phe Leu Arg Pro Pro Leu Arg Arg Arg Phe Leu
            20                  25                  30

tct ttc tct cca cat act ctg tgc cga gag cag ata cgt tgc gtg aag      144
Ser Phe Ser Pro His Thr Leu Cys Arg Glu Gln Ile Arg Cys Val Lys
        35                  40                  45

gag cgg aag ttt ttt gcc aca acg gca aaa aaa ctc aaa caa cca aaa      192
Glu Arg Lys Phe Phe Ala Thr Thr Ala Lys Lys Leu Lys Gln Pro Lys
    50                  55                  60

agt att cca gag gaa aaa gac tat gtt aat att atg tgg tgg aaa gag      240
Ser Ile Pro Glu Glu Lys Asp Tyr Val Asn Ile Met Trp Trp Lys Glu
65                  70                  75                  80

aga atg gaa ttc ttg aga aag cct tct tcc gct ctt ctg gct aag agg      288
Arg Met Glu Phe Leu Arg Lys Pro Ser Ser Ala Leu Leu Ala Lys Arg
                85                  90                  95

ctt aca tat tgt aac ttg ctg ggt gtg gat ccg agt ttg aga aat gga      336
Leu Thr Tyr Cys Asn Leu Leu Gly Val Asp Pro Ser Leu Arg Asn Gly
            100                 105                 110

agt ctt aaa gag gga aca ctt aac tcg gag atg ttg cag ttc aag tca      384
Ser Leu Lys Glu Gly Thr Leu Asn Ser Glu Met Leu Gln Phe Lys Ser
        115                 120                 125

aaa ttt cca cgt gaa gtt ttg ctc tgt aga gta ggt gat ttt tat gaa      432
Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val Gly Asp Phe Tyr Glu
    130                 135                 140

gct att gga ttc gat gct tgt att ctt gtg gaa tat gct ggt tta aat      480
Ala Ile Gly Phe Asp Ala Cys Ile Leu Val Glu Tyr Ala Gly Leu Asn
145                 150                 155                 160

cca ttt ggt ggc ctg cac tca gat agt ata cca aaa gct ggt tgt cca      528
Pro Phe Gly Gly Leu His Ser Asp Ser Ile Pro Lys Ala Gly Cys Pro
                165                 170                 175

gtt gtg aat cta aga cag acg ctt gat gat ctc aca cgt aat ggt ttc      576
Val Val Asn Leu Arg Gln Thr Leu Asp Asp Leu Thr Arg Asn Gly Phe
            180                 185                 190

tct gtg tgc gtc gtg gag gaa gtt cag ggt cca act caa gct cgt gct      624
Ser Val Cys Val Val Glu Glu Val Gln Gly Pro Thr Gln Ala Arg Ala
        195                 200                 205

cgt aag agt cga ttt ata tca ggg cat gca cat cca ggc agt ccc tat      672
Arg Lys Ser Arg Phe Ile Ser Gly His Ala His Pro Gly Ser Pro Tyr
    210                 215                 220

gtt ttt ggc ctt gtt gna gat gat caa gat ctt gat ttt cca gaa cca      720
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Val Phe Gly Leu Val Xaa Asp Asp Gln Asp Leu Asp Phe Pro Glu Pro
225                 230                 235                 240

atg cct gtt gtt gga ata tcc cgt tca gcg aag ggg tat tgc att atc      768
Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys Gly Tyr Cys Ile Ile
                245                 250                 255

tct gtt tac gag act atg aag act tac tct gtg gaa gat ggc cta act      816
Ser Val Tyr Glu Thr Met Lys Thr Tyr Ser Val Glu Asp Gly Leu Thr
            260                 265                 270

gaa gaa gcc gta gtc acc aaa ctt cgt act tgt cga tgc cat cat ttt      864
Glu Glu Ala Val Val Thr Lys Leu Arg Thr Cys Arg Cys His His Phe
        275                 280                 285

ttt ttg cat aat tca ttg aag aac aat tcc tca gga aca tcg cgt tgg      912
Phe Leu His Asn Ser Leu Lys Asn Asn Ser Ser Gly Thr Ser Arg Trp
    290                 295                 300

gga gag ttt ggt gaa ggt gga ctt ttg tgg gga gaa tgt aat gct aga      960
Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly Glu Cys Asn Ala Arg
305                 310                 315                 320

cag cag gaa tgg ttg gat ggc aat cct atc gat gag ctt ttg ttc aag     1008
Gln Gln Glu Trp Leu Asp Gly Asn Pro Ile Asp Glu Leu Leu Phe Lys
                325                 330                 335

gta aaa gag ctt tat ggt ctc aat gat gac att cca ttc aga aat gtc     1056
Val Lys Glu Leu Tyr Gly Leu Asn Asp Asp Ile Pro Phe Arg Asn Val
            340                 345                 350

act gtt gtt tca gaa aat agg ccc cgt cct tta cac ctt gga act gcc     1104
Thr Val Val Ser Glu Asn Arg Pro Arg Pro Leu His Leu Gly Thr Ala
        355                 360                 365

aca caa att ggt gct att cca acc gaa ggg att cca tgt ttg tta aag     1152
Thr Gln Ile Gly Ala Ile Pro Thr Glu Gly Ile Pro Cys Leu Leu Lys
    370                 375                 380

gtg ttg ctt cct cct cat tgc agt ggt cta cca gtc ctg tat att agg     1200
Val Leu Leu Pro Pro His Cys Ser Gly Leu Pro Val Leu Tyr Ile Arg
385                 390                 395                 400

gat ctt ctt tta aat cca cca gcc tat gag att tct tca gac ata caa     1248
Asp Leu Leu Leu Asn Pro Pro Ala Tyr Glu Ile Ser Ser Asp Ile Gln
                405                 410                 415

gag gca tgc aga ctt atg atg agt gtc aca tgt tca att cct gat ttt     1296
Glu Ala Cys Arg Leu Met Met Ser Val Thr Cys Ser Ile Pro Asp Phe
            420                 425                 430

acc tgt att tca tct gca aag ctg gtc aag ctg ctt gag ttg agg gag     1344
Thr Cys Ile Ser Ser Ala Lys Leu Val Lys Leu Leu Glu Leu Arg Glu
        435                 440                 445

gca aat cac gtt gag ttc tgc aaa ata aag agc atg gtc gaa gag ata     1392
Ala Asn His Val Glu Phe Cys Lys Ile Lys Ser Met Val Glu Glu Ile
    450                 455                 460

ctg cag ttg tat aga aat tca gag ctt cgt gct atw gta gag tta ctg     1440
Leu Gln Leu Tyr Arg Asn Ser Glu Leu Arg Ala Xaa Val Glu Leu Leu
465                 470                 475                 480
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atg gat cct act tgg gtg gca act ggg ttg aaa gtt gat ttt gat aca      1488
Met Asp Pro Thr Trp Val Ala Thr Gly Leu Lys Val Asp Phe Asp Thr
                485                 490                 495

cta gta aat gaa tgt gga aag att tct tgt aga atc agt gaa ata ata      1536
Leu Val Asn Glu Cys Gly Lys Ile Ser Cys Arg Ile Ser Glu Ile Ile
            500                 505                 510

tcc gta cat ggt gaa aat gat caa aag att agt tcc tat cct atc atc      1584
Ser Val His Gly Glu Asn Asp Gln Lys Ile Ser Ser Tyr Pro Ile Ile
        515                 520                 525

cca aat gat ttc ttt gaa gat atg gag ttg ttg tgg aaa ggc cgt gtc      1632
Pro Asn Asp Phe Phe Glu Asp Met Glu Leu Leu Trp Lys Gly Arg Val
    530                 535                 540

aag agg atc cat ttg gag gaa gca tat gca gaa gta gaa aag gct gcg      1680
Lys Arg Ile His Leu Glu Glu Ala Tyr Ala Glu Val Glu Lys Ala Ala
545                 550                 555                 560

gat gct tta tct tta gcc ata aca gaa gat ttc cta cct att att tca      1728
Asp Ala Leu Ser Leu Ala Ile Thr Glu Asp Phe Leu Pro Ile Ile Ser
                565                 570                 575

aga ata agg gcc acg atg gcc cca ctt gga gga act aaa ggg gag att      1776
Arg Ile Arg Ala Thr Met Ala Pro Leu Gly Gly Thr Lys Gly Glu Ile
            580                 585                 590

ttg tat gcc cgt gag cat gga gct gta tgg ttt aag gga aag aga ttt      1824
Leu Tyr Ala Arg Glu His Gly Ala Val Trp Phe Lys Gly Lys Arg Phe
        595                 600                 605

gta cca act gtt tgg gct gga acc gct gga gaa gaa caa att aag caa      1872
Val Pro Thr Val Trp Ala Gly Thr Ala Gly Glu Glu Gln Ile Lys Gln
    610                 615                 620

ctc aga cct gct cta gat tca aag ggg aag aag gtt gga gaa gaa tgg      1920
Leu Arg Pro Ala Leu Asp Ser Lys Gly Lys Lys Val Gly Glu Glu Trp
625                 630                 635                 640

ttc act aca atg agg gtg gaa gat gca ata gct agg tat cac gag gca      1968
Phe Thr Thr Met Arg Val Glu Asp Ala Ile Ala Arg Tyr His Glu Ala
                645                 650                 655

agt gct agg gca aag tca agg gtc ttg gaa ttg cta agg gga ctt tct      2016
Ser Ala Arg Ala Lys Ser Arg Val Leu Glu Leu Leu Arg Gly Leu Ser
            660                 665                 670

tct gaa tta cta tct aag atc aat atc ctt atc ttt gca tct gtc ttg      2064
Ser Glu Leu Leu Ser Lys Ile Asn Ile Leu Ile Phe Ala Ser Val Leu
        675                 680                 685

aat gtg ata gca aaa tca tta ttt tct cat gtg agt gaa gga aga aga      2112
Asn Val Ile Ala Lys Ser Leu Phe Ser His Val Ser Glu Gly Arg Arg
    690                 695                 700

aga aat tgg att ttc cca aca atc aca caa ttt aac aaa tgt cag gac      2160
Arg Asn Trp Ile Phe Pro Thr Ile Thr Gln Phe Asn Lys Cys Gln Asp
705                 710                 715                 720

aca gag gca ctt aat gga act gat gga atg aag ata att ggt cta tct      2208
Thr Glu Ala Leu Asn Gly Thr Asp Gly Met Lys Ile Ile Gly Leu Ser
                725                 730                 735
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cct tat tgg ttt gat gca gca cga ggg act ggt gta cag gat aca gta      2256
Pro Tyr Trp Phe Asp Ala Ala Arg Gly Thr Gly Val Gln Asp Thr Val
            740                 745                 750

gat atg cag tcc atg ttt ctt tta aca ggt cca aat ggt ggg ggc aaa      2304
Asp Met Gln Ser Met Phe Leu Leu Thr Gly Pro Asn Gly Gly Gly Lys
        755                 760                 765

tca agc ttg ctg cgt tcg ttg tgt gca gct gca ttg cta gga atg tgt      2352
Ser Ser Leu Leu Arg Ser Leu Cys Ala Ala Ala Leu Leu Gly Met Cys
    770                 775                 780

ggg ttc atg gtt cca gct gaa tca gct gtc att cct cat ttt gac tca      2400
Gly Phe Met Val Pro Ala Glu Ser Ala Val Ile Pro His Phe Asp Ser
785                 790                 795                 800

att atg ctg cat atg aaa tca tat gat agt cct gtt gat gga aaa agt      2448
Ile Met Leu His Met Lys Ser Tyr Asp Ser Pro Val Asp Gly Lys Ser
                805                 810                 815

tca ttt cag att gaa atg tct gaa att cgg tct ctg att act ggt gcc      2496
Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Ile Thr Gly Ala
            820                 825                 830

act tca aga agt ctt gta ctt ata gat gaa ata tgt cga gga aca gaa      2544
Thr Ser Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg Gly Thr Glu
        835                 840                 845

aca gca aaa ggg aca tgt att gct gga agt gtc ata gaa acc ctg gac      2592
Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Val Ile Glu Thr Leu Asp
    850                 855                 860

gaa att ggc tgt ttg gga att gta tca acc cac ttg cat gga ata ttt      2640
Glu Ile Gly Cys Leu Gly Ile Val Ser Thr His Leu His Gly Ile Phe
865                 870                 875                 880

gat tta ccc ctg aaa atc aag aag acc gtg tat aaa gca atg gga gct      2688
Asp Leu Pro Leu Lys Ile Lys Lys Thr Val Tyr Lys Ala Met Gly Ala
                885                 890                 895

gaa tat gtt gac ggt caa cca ata cca act tgg aaa ctc att gat ggg      2736
Glu Tyr Val Asp Gly Gln Pro Ile Pro Thr Trp Lys Leu Ile Asp Gly
            900                 905                 910

atc tgt aaa gag agt cta gca ttt gaa aca gct cag aga gaa gga att      2784
Ile Cys Lys Glu Ser Leu Ala Phe Glu Thr Ala Gln Arg Glu Gly Ile
        915                 920                 925

cca gaa ata tta atc caa aga gca gaa gaa ttg tat aat tca gct tac      2832
Pro Glu Ile Leu Ile Gln Arg Ala Glu Glu Leu Tyr Asn Ser Ala Tyr
    930                 935                 940

ggg aat cag ata cca agg aag ata gac caa ata aga cct ctt cgt tca      2880
Gly Asn Gln Ile Pro Arg Lys Ile Asp Gln Ile Arg Pro Leu Arg Ser
945                 950                 955                 960

gat att gac ctc aat agc aca gat aac agt tct gac caa tta aat ggt      2928
Asp Ile Asp Leu Asn Ser Thr Asp Asn Ser Ser Asp Gln Leu Asn Gly
                965                 970                 975

aca aga caa ata gct ttg gat tct agc aca aag tta atg cat cga atg      2976
Thr Arg Gln Ile Ala Leu Asp Ser Ser Thr Lys Leu Met His Arg Met
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            980                 985                 990

gga att tca agc aag aaa ctt gaa  gat gct atc tgt ctt  atc tgt gag   3024
Gly Ile Ser Ser Lys Lys Leu Glu  Asp Ala Ile Cys Leu  Ile Cys Glu
        995                1000                1005

aag aag  tta att gag ctg tat  aaa atg aaa aat ccg  tca gaa atg      3069
Lys Lys  Leu Ile Glu Leu Tyr  Lys Met Lys Asn Pro  Ser Glu Met
    1010                1015                1020

cca atg  gtg aat tgc gtt ctt  att gct gcc agg gaa  cag ccg gct      3114
Pro Met  Val Asn Cys Val Leu  Ile Ala Ala Arg Glu  Gln Pro Ala
    1025                1030                1035

cca tca  aca att ggt gct tca  agt gtc tat ata atg  cta aga cct      3159
Pro Ser  Thr Ile Gly Ala Ser  Ser Val Tyr Ile Met  Leu Arg Pro
    1040                1045                1050

gac aaa  aag ttg tat gtt gga  cag act gat gat ctt  gag ggc aga      3204
Asp Lys  Lys Leu Tyr Val Gly  Gln Thr Asp Asp Leu  Glu Gly Arg
    1055                1060                1065

gta cgt  gct cat cgc ttg aag  gag gga atg gaa aac  gcg tca ttc      3249
Val Arg  Ala His Arg Leu Lys  Glu Gly Met Glu Asn  Ala Ser Phe
    1070                1075                1080

cta tat  ttc tta gtc tct ggc  aag agc atc gcc tgc  caa ttg gaa      3294
Leu Tyr  Phe Leu Val Ser Gly  Lys Ser Ile Ala Cys  Gln Leu Glu
    1085                1090                1095

act ctt  cta ata aat caa ctt  cct aat cat ggt ttt  cag cta aca      3339
Thr Leu  Leu Ile Asn Gln Leu  Pro Asn His Gly Phe  Gln Leu Thr
    1100                1105                1110

aac gtt  gct gat ggt aag cat  cgt aat ttt ggc a                    3373
Asn Val  Ala Asp Gly Lys His  Arg Asn Phe Gly
    1115                1120


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<211>  1124
<212>  PRT
<213>  Lycopersicon esculentum

<220>
<221>  misc_feature
<222>  (230)..(230)
<223>  The 'Xaa' at location 230 stands for Glu, Gly, Ala, or Val.

<220>
<221>  misc_feature
<222>  (476)..(476)
<223>  The 'Xaa' at location 476 stands for Ile.

<400>  40

Met Tyr Trp Val Thr Ala Lys Asn Val Val Val Ser Val Pro Arg Trp
1               5                  10                  15


Arg Ser Leu Ser Leu Phe Leu Arg Pro Pro Leu Arg Arg Arg Phe Leu
            20                  25                  30
```

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Ser Phe Ser Pro His Thr Leu Cys Arg Glu Gln Ile Arg Cys Val Lys
        35                  40                  45

Glu Arg Lys Phe Phe Ala Thr Thr Ala Lys Lys Leu Lys Gln Pro Lys
    50                  55                  60

Ser Ile Pro Glu Glu Lys Asp Tyr Val Asn Ile Met Trp Trp Lys Glu
65                  70                  75                  80

Arg Met Glu Phe Leu Arg Lys Pro Ser Ser Ala Leu Leu Ala Lys Arg
                85                  90                  95

Leu Thr Tyr Cys Asn Leu Leu Gly Val Asp Pro Ser Leu Arg Asn Gly
            100                 105                 110

Ser Leu Lys Glu Gly Thr Leu Asn Ser Glu Met Leu Gln Phe Lys Ser
        115                 120                 125

Lys Phe Pro Arg Glu Val Leu Leu Cys Arg Val Gly Asp Phe Tyr Glu
    130                 135                 140

Ala Ile Gly Phe Asp Ala Cys Ile Leu Val Glu Tyr Ala Gly Leu Asn
145                 150                 155                 160

Pro Phe Gly Gly Leu His Ser Asp Ser Ile Pro Lys Ala Gly Cys Pro
                165                 170                 175

Val Val Asn Leu Arg Gln Thr Leu Asp Asp Leu Thr Arg Asn Gly Phe
            180                 185                 190

Ser Val Cys Val Val Glu Glu Val Gln Gly Pro Thr Gln Ala Arg Ala
        195                 200                 205

Arg Lys Ser Arg Phe Ile Ser Gly His Ala His Pro Gly Ser Pro Tyr
    210                 215                 220

Val Phe Gly Leu Val Xaa Asp Asp Gln Asp Leu Asp Phe Pro Glu Pro
225                 230                 235                 240

Met Pro Val Val Gly Ile Ser Arg Ser Ala Lys Gly Tyr Cys Ile Ile
                245                 250                 255

Ser Val Tyr Glu Thr Met Lys Thr Tyr Ser Val Glu Asp Gly Leu Thr
            260                 265                 270

Glu Glu Ala Val Val Thr Lys Leu Arg Thr Cys Arg Cys His His Phe
        275                 280                 285
```

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Phe Leu His Asn Ser Leu Lys Asn Asn Ser Ser Gly Thr Ser Arg Trp
    290                 295                 300

Gly Glu Phe Gly Glu Gly Gly Leu Leu Trp Gly Glu Cys Asn Ala Arg
305                 310                 315                 320

Gln Gln Glu Trp Leu Asp Gly Asn Pro Ile Asp Glu Leu Leu Phe Lys
                325                 330                 335

Val Lys Glu Leu Tyr Gly Leu Asn Asp Asp Ile Pro Phe Arg Asn Val
            340                 345                 350

Thr Val Val Ser Glu Asn Arg Pro Arg Pro Leu His Leu Gly Thr Ala
        355                 360                 365

Thr Gln Ile Gly Ala Ile Pro Thr Glu Gly Ile Pro Cys Leu Leu Lys
    370                 375                 380

Val Leu Leu Pro Pro His Cys Ser Gly Leu Pro Val Leu Tyr Ile Arg
385                 390                 395                 400

Asp Leu Leu Leu Asn Pro Pro Ala Tyr Glu Ile Ser Ser Asp Ile Gln
                405                 410                 415

Glu Ala Cys Arg Leu Met Met Ser Val Thr Cys Ser Ile Pro Asp Phe
            420                 425                 430

Thr Cys Ile Ser Ser Ala Lys Leu Val Lys Leu Leu Glu Leu Arg Glu
        435                 440                 445

Ala Asn His Val Glu Phe Cys Lys Ile Lys Ser Met Val Glu Glu Ile
    450                 455                 460

Leu Gln Leu Tyr Arg Asn Ser Glu Leu Arg Ala Xaa Val Glu Leu Leu
465                 470                 475                 480

Met Asp Pro Thr Trp Val Ala Thr Gly Leu Lys Val Asp Phe Asp Thr
                485                 490                 495

Leu Val Asn Glu Cys Gly Lys Ile Ser Cys Arg Ile Ser Glu Ile Ile
            500                 505                 510

Ser Val His Gly Glu Asn Asp Gln Lys Ile Ser Ser Tyr Pro Ile Ile
        515                 520                 525

Pro Asn Asp Phe Phe Glu Asp Met Glu Leu Leu Trp Lys Gly Arg Val
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530 535 540

Lys Arg Ile His Leu Glu Glu Ala Tyr Ala Glu Val Glu Lys Ala Ala
545 550 555 560

Asp Ala Leu Ser Leu Ala Ile Thr Glu Asp Phe Leu Pro Ile Ile Ser
565 570 575

Arg Ile Arg Ala Thr Met Ala Pro Leu Gly Gly Thr Lys Gly Glu Ile
580 585 590

Leu Tyr Ala Arg Glu His Gly Ala Val Trp Phe Lys Gly Lys Arg Phe
595 600 605

Val Pro Thr Val Trp Ala Gly Thr Ala Gly Glu Glu Gln Ile Lys Gln
610 615 620

Leu Arg Pro Ala Leu Asp Ser Lys Gly Lys Lys Val Gly Glu Glu Trp
625 630 635 640

Phe Thr Thr Met Arg Val Glu Asp Ala Ile Ala Arg Tyr His Glu Ala
645 650 655

Ser Ala Arg Ala Lys Ser Arg Val Leu Glu Leu Leu Arg Gly Leu Ser
660 665 670

Ser Glu Leu Leu Ser Lys Ile Asn Ile Leu Ile Phe Ala Ser Val Leu
675 680 685

Asn Val Ile Ala Lys Ser Leu Phe Ser His Val Ser Glu Gly Arg Arg
690 695 700

Arg Asn Trp Ile Phe Pro Thr Ile Thr Gln Phe Asn Lys Cys Gln Asp
705 710 715 720

Thr Glu Ala Leu Asn Gly Thr Asp Gly Met Lys Ile Ile Gly Leu Ser
725 730 735

Pro Tyr Trp Phe Asp Ala Ala Arg Gly Thr Gly Val Gln Asp Thr Val
740 745 750

Asp Met Gln Ser Met Phe Leu Leu Thr Gly Pro Asn Gly Gly Gly Lys
755 760 765

Ser Ser Leu Leu Arg Ser Leu Cys Ala Ala Ala Leu Leu Gly Met Cys
770 775 780

```
Gly Phe Met Val Pro Ala Glu Ser Ala Val Ile Pro His Phe Asp Ser
785                 790                 795                 800

Ile Met Leu His Met Lys Ser Tyr Asp Ser Pro Val Asp Gly Lys Ser
                805                 810                 815

Ser Phe Gln Ile Glu Met Ser Glu Ile Arg Ser Leu Ile Thr Gly Ala
            820                 825                 830

Thr Ser Arg Ser Leu Val Leu Ile Asp Glu Ile Cys Arg Gly Thr Glu
        835                 840                 845

Thr Ala Lys Gly Thr Cys Ile Ala Gly Ser Val Ile Glu Thr Leu Asp
    850                 855                 860

Glu Ile Gly Cys Leu Gly Ile Val Ser Thr His Leu His Gly Ile Phe
865                 870                 875                 880

Asp Leu Pro Leu Lys Ile Lys Lys Thr Val Tyr Lys Ala Met Gly Ala
                885                 890                 895

Glu Tyr Val Asp Gly Gln Pro Ile Pro Thr Trp Lys Leu Ile Asp Gly
            900                 905                 910

Ile Cys Lys Glu Ser Leu Ala Phe Glu Thr Ala Gln Arg Glu Gly Ile
        915                 920                 925

Pro Glu Ile Leu Ile Gln Arg Ala Glu Glu Leu Tyr Asn Ser Ala Tyr
    930                 935                 940

Gly Asn Gln Ile Pro Arg Lys Ile Asp Gln Ile Arg Pro Leu Arg Ser
945                 950                 955                 960

Asp Ile Asp Leu Asn Ser Thr Asp Asn Ser Ser Asp Gln Leu Asn Gly
                965                 970                 975

Thr Arg Gln Ile Ala Leu Asp Ser Ser Thr Lys Leu Met His Arg Met
            980                 985                 990

Gly Ile Ser Ser Lys Lys Leu Glu  Asp Ala Ile Cys Leu  Ile Cys Glu
        995                 1000                1005

Lys Lys  Leu Ile Glu Leu Tyr  Lys Met Lys Asn Pro  Ser Glu Met
    1010                1015                1020

Pro Met  Val Asn Cys Val Leu  Ile Ala Ala Arg Glu  Gln Pro Ala
    1025                1030                1035
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Pro Ser Thr Ile Gly Ala Ser Ser Val Tyr Ile Met Leu Arg Pro
1040 1045 1050

Asp Lys Lys Leu Tyr Val Gly Gln Thr Asp Asp Leu Glu Gly Arg
1055 1060 1065

Val Arg Ala His Arg Leu Lys Glu Gly Met Glu Asn Ala Ser Phe
1070 1075 1080

Leu Tyr Phe Leu Val Ser Gly Lys Ser Ile Ala Cys Gln Leu Glu
1085 1090 1095

Thr Leu Leu Ile Asn Gln Leu Pro Asn His Gly Phe Gln Leu Thr
1100 1105 1110

Asn Val Ala Asp Gly Lys His Arg Asn Phe Gly
1115 1120

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<211> 622
<212> DNA
<213> Triticum aestivum

<400> 41
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gtatcagtta gctcctgcct cctataagcc aaaaaaacag ataaggaaat caaagatgaa 120

gctccactcc cctttggcct ctacgagtta aaactggatg ttcagtgggt cagttcagtg 180

tgcagccatg gcttctccag aggttacaga cataccaaag ttccgatgct tgccatctgc 240

cttgttggtg agcttaaaac ctttcgtggg tagctgattt atgagaagag tctccagttg 300

gcaggcaaca ctcttgccag gaacaatgat gtataatatt gtggcatcct gcataccttc 360

cttcgatcta tgagcaccaa gacggcccac aagatcatcc gtctgtccaa catagagctt 420

gttgtcacgt ctgatgatga tatagatgct ggacctccca acagttgaag gtggcggttg 480

ctccctagca cctacagtaa cgcagaccac ctcaaccagt tctgagatgc ttctcttgtt 540

gtagagatcc aacagtttat ctttgcatat tgtggtaaca atgctctcga catcctttgg 600

cagcagtcca gtagcacctg ac 622

<210> 42
<211> 148
<212> PRT
<213> Triticum aestivum

<400> 42

Ser Gly Ala Thr Gly Leu Leu Pro Lys Asp Val Glu Ser Ile Val Thr
1 5 10 15

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Thr Ile Cys Lys Asp Lys Leu Leu Asp Leu Tyr Asn Lys Arg Ser Ile
            20                  25                  30

Ser Glu Leu Val Glu Val Val Cys Val Thr Val Gly Ala Arg Glu Gln
        35                  40                  45

Pro Pro Pro Ser Thr Val Gly Arg Ser Ser Ile Tyr Ile Ile Ile Arg
    50                  55                  60

Arg Asp Asn Lys Leu Tyr Val Gly Gln Thr Asp Asp Leu Val Gly Arg
65                  70                  75                  80

Leu Gly Ala His Arg Ser Lys Glu Gly Met Gln Asp Ala Thr Ile Leu
                85                  90                  95

Tyr Ile Ile Val Pro Gly Lys Ser Val Ala Cys Gln Leu Glu Thr Leu
            100                 105                 110

Leu Ile Asn Gln Leu Pro Thr Lys Gly Phe Lys Leu Thr Asn Lys Ala
        115                 120                 125

Asp Gly Lys His Arg Asn Phe Gly Met Ser Val Thr Ser Gly Glu Ala
    130                 135                 140

Met Ala Ala His
145
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<210> 43
<211> 523
<212> DNA
<213> Zinnia elegans

<400> 43
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ggataaggca gctgaagcct tatccttagc tgtaacggag gattttcttc ctataatttg 120

tagaataaaa gctaccacag caccacttgg aggaccaaaa ggggaaattt tgtatgttcg 180

ggaacacaaa gctatatggt tcaagggcaa acgttttgta ccaaccatag gggctaatac 240

gcctgtagaa aagcaaatta aacaacttaa gccctctgta gattcaaagg gtagaaaagt 300

tggagaggaa tggtttacca caagtaaagt ggaggatgca ctctcaaggt accatgaagc 360

tggtgcaaaa gcgaagtcca tggtgttaga gttattgagg ggactgtctg ctgaattgca 420

agctgaaatt aatgttctcg tgtttgcctc catgttgctt attatcgcaa aggcattgtt 480

tgctcatgtg aggtattcta tatctgaatt ttttgaccgt tgt 523

<210> 44
<211> 174
<212> PRT
<213> Zinnia elegans

<400> 44

Glu Ser Ser Trp Lys Asn Arg Val Lys Lys Ile His Leu Lys Glu Ala
1 5 10 15

Tyr Glu Glu Val Asp Lys Ala Ala Glu Ala Leu Ser Leu Ala Val Thr
20 25 30

Glu Asp Phe Leu Pro Ile Ile Cys Arg Ile Lys Ala Thr Thr Ala Pro
35 40 45

Leu Gly Gly Pro Lys Gly Glu Ile Leu Tyr Val Arg Glu His Lys Ala
50 55 60

Ile Trp Phe Lys Gly Lys Arg Phe Val Pro Thr Ile Gly Ala Asn Thr
65 70 75 80

Pro Val Glu Lys Gln Ile Lys Gln Leu Lys Pro Ser Val Asp Ser Lys
85 90 95

Gly Arg Lys Val Gly Glu Glu Trp Phe Thr Thr Ser Lys Val Glu Asp
100 105 110

Ala Leu Ser Arg Tyr His Glu Ala Gly Ala Lys Ala Lys Ser Met Val
115 120 125

Leu Glu Leu Leu Arg Gly Leu Ser Ala Glu Leu Gln Ala Glu Ile Asn
130 135 140

Val Leu Val Phe Ala Ser Met Leu Leu Ile Ile Ala Lys Ala Leu Phe
145 150 155 160

Ala His Val Arg Tyr Ser Ile Ser Glu Phe Phe Asp Arg Cys
165 170

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<211> 3381
<212> DNA
<213> Phaseolus vulgaris

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ataaatggac gtgtcaagaa tgtatcaact tatatggata ataacagggt ttcaagggga 180

agtagtagga ccaccaagaa gccaaaagta ccaaataatg ttttagatga caaagatctt 240

cctcacatat cgtggtggaa ggagaggttg caaatgtgca aaaagttttc gactgtccag 300

ctaattcaaa ggcttgaatt ttctaatttg cttggtctgg attccaaatt gaaaaatgga 360

agtgtgaagg aaggaacact caactgggaa atgttgcagt tcaagtcaaa atttccacgt 420

caagtattac tctgcagagt aggggaattc tatgaagcat ggggaataga tgcttgtgtt 480

ctagttgaat atgctggttt aaatccctgt ggtggtctcc aatcagatag tgttccaagg 540

gctggttgtc ctgttgtgaa tcttcgacag actttagatg atctgaccca aaatggttat 600

tcagtgtgca tcattgagga agttcagggc ccaactcaag ctcgatccag gaaacgccgc 660

tttatatctg ggcatgctca tcctggaaat ccctatgtat atggacttgc tgcagttgat 720

catgatctta actttcctga gccaatgcct gtaataggaa tatctcattc tgcgaggggc 780

tattgcatta acatggtgct agagactatg aaaacatact cttatgaaga ttgcttgaca 840

gaggaagcaa ttgtgacaaa gcttcgtact tgtcaatatc atcacttatt cttgcataca 900

tctttgacgc aggattcttg tggcaccagc aaatggggag aattcggtga ggggggtctc 960

ttatggggag aatgtagttc tagacatttt gaatggtttg atggcagccc tctctctgat 1020

ctcttggtca aggtaaagga gctttatggt cttgatgatg aggttacttt tcgaaacaca 1080

accgtatctt cgagacatag ggctcgacct ttaacccttg gaacatctac tcaaattggt 1140

gccattcata cggaaggaat accttctttg ttaaaggtct tactttcacc aagttgcaat 1200

ggattaccgg ttctgtatat aaggaatctt ctcttgaatc ctccttctta tgagatcgca 1260

tccaaaattc aggaaacatg caaacttatg agcagtttaa cgtgctcaat tccagaattt 1320

acgtgtgttt cttcagcaaa gcttgtaaag ctacttgagt ggagggaggt caaccatatg 1380

gaattttgta gaataaagaa tgtgcttgat gagattttgc atatgtacaa aacctctgag 1440

ctcaatgaaa tattgaaaaa tttaattgat ccaacatggg cgacaactgg gttagacatc 1500

gactttgaaa cactggtttc tggatgtgaa gttgcatcta gtaagatcag tgaaataatc 1560

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cctgttgttt ctagagtaaa ggctactata gccccacttg gaggtcctag gggagaaatt 1800

tcttatgctc gtgagcatga ggcagtttgg ttcagaggca aacgctttac gccgagtttg 1860

tggtctggta gccctgggga ggaacaaatt aaacagctta ggcatgcttt agattctaaa 1920

ggtaaaaggg taggggagga atggtttact acaccgaagg ttgaggctgc attaacaagg 1980

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actgaattgc attacagtat aaacattctt gtcttttcat ccacgttgct tgttattacc 2100

aaagctttat tcgctcatgc aagtgaaggg agaagaagga gatgggtttt tccaacactt 2160

gcagaatcga atgggtttga ggatgtgaaa tcttcggaca aaatccatgg gatgaagata 2220

gttggtttag caccttattg gttccacata gcagaaggta ttgtgcgtaa tgatgttgat 2280

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actcacttgc atggaatatt tactttgccc ctcaacatca aaagcactgt gcacaaagca 2700

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tgtaaagaaa gtcttgcttt tgaaactgcc attagggaag gaattcctga gcctattata 2820

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aagttttcta cttgcaacaa tttgaataat ttgaatacaa caagtcttta ttctaaaggg 2940

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gtgatatgcc aggattatat aatggaacgg aaaaacaaaa agattgcatt ggagcttcct 3060

gagataaaat gtctcctaat cggtaagagg gagcagccac ctccatctgt tgtaggttct 3120

tcaagcgtct atgtgatttt cacgccagat aagaaactct acgtaggaga gacggatgat 3180

ctagagggcc gggttcgaag acatagattg aaagaaggta tggatgaagc atcatttctt 3240

tattttcttg ttccgggaaa aagcttggca tgccaatttg aatctctgct catcaaccag 3300

ctttctagtc aaggcttcca actgagcaac atggctgatg gtaaacatag gaattttggc 3360

acttccaacc tctatgcata a 3381

<210> 46
<211> 3381
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> CDS
<222> (1)..(3381)

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Met Tyr Arg Ala Val Thr Arg Asn Val Ala Val Phe Leu Pro Arg Cys
1 5 10 15

cgc tct ctc tcg cac ttc tct cat tcg cta ttt ccc ttc ttc att tca 96
Arg Ser Leu Ser His Phe Ser His Ser Leu Phe Pro Phe Phe Ile Ser

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            20                  25                  30

tcc ctt ccc tct cgc ttc ctt cga ata aat gga cgt gtc aag aat gta      144
Ser Leu Pro Ser Arg Phe Leu Arg Ile Asn Gly Arg Val Lys Asn Val
        35                  40                  45

tca act tat atg gat aat aac agg gtt tca agg gga agt agt agg acc      192
Ser Thr Tyr Met Asp Asn Asn Arg Val Ser Arg Gly Ser Ser Arg Thr
    50                  55                  60

acc aag aag cca aaa gta cca aat aat gtt tta gat gac aaa gat ctt      240
Thr Lys Lys Pro Lys Val Pro Asn Asn Val Leu Asp Asp Lys Asp Leu
65                  70                  75                  80

cct cac ata tcg tgg tgg aag gag agg ttg caa atg tgc aaa aag ttt      288
Pro His Ile Ser Trp Trp Lys Glu Arg Leu Gln Met Cys Lys Lys Phe
                85                  90                  95

tcg act gtc cag cta att caa agg ctt gaa ttt tct aat ttg ctt ggt      336
Ser Thr Val Gln Leu Ile Gln Arg Leu Glu Phe Ser Asn Leu Leu Gly
            100                 105                 110

ctg gat tcc aaa ttg aaa aat gga agt gtg aag gaa gga aca ctc aac      384
Leu Asp Ser Lys Leu Lys Asn Gly Ser Val Lys Glu Gly Thr Leu Asn
        115                 120                 125

tgg gaa atg ttg cag ttc aag tca aaa ttt cca cgt caa gta tta ctc      432
Trp Glu Met Leu Gln Phe Lys Ser Lys Phe Pro Arg Gln Val Leu Leu
    130                 135                 140

tgc aga gta ggg gaa ttc tat gaa gca tgg gga ata gat gct tgt gtt      480
Cys Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Val
145                 150                 155                 160

cta gtt gaa tat gct ggt tta aat ccc tgt ggt ggt ctc caa tca gat      528
Leu Val Glu Tyr Ala Gly Leu Asn Pro Cys Gly Gly Leu Gln Ser Asp
                165                 170                 175

agt gtt cca agg gct ggt tgt cct gtt gtg aat ctt cga cag act tta      576
Ser Val Pro Arg Ala Gly Cys Pro Val Val Asn Leu Arg Gln Thr Leu
            180                 185                 190

gat gat ctg acc caa aat ggt tat tca gtg tgc atc att gag gaa gtt      624
Asp Asp Leu Thr Gln Asn Gly Tyr Ser Val Cys Ile Ile Glu Glu Val
        195                 200                 205

cag ggc cca act caa gct cga tcc agg aaa cgc cgc ttt ata tct ggg      672
Gln Gly Pro Thr Gln Ala Arg Ser Arg Lys Arg Arg Phe Ile Ser Gly
    210                 215                 220

cat gct cat cct gga aat ccc tat gta tat gga ctt gct gca gtt gat      720
His Ala His Pro Gly Asn Pro Tyr Val Tyr Gly Leu Ala Ala Val Asp
225                 230                 235                 240

cat gat ctt aac ttt cct gag cca atg cct gta ata gga ata tct cat      768
His Asp Leu Asn Phe Pro Glu Pro Met Pro Val Ile Gly Ile Ser His
                245                 250                 255

tct gcg agg ggc tat tgc att aac atg gtg cta gag act atg aaa aca      816
Ser Ala Arg Gly Tyr Cys Ile Asn Met Val Leu Glu Thr Met Lys Thr
            260                 265                 270

tac tct tat gaa gat tgc ttg aca gag gaa gca att gtg aca aag ctt      864
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Tyr Ser Tyr Glu Asp Cys Leu Thr Glu Glu Ala Ile Val Thr Lys Leu
        275                 280                 285

cgt act tgt caa tat cat cac tta ttc ttg cat aca tct ttg acg cag      912
Arg Thr Cys Gln Tyr His His Leu Phe Leu His Thr Ser Leu Thr Gln
    290                 295                 300

gat tct tgt ggc acc agc aaa tgg gga gaa ttc ggt gag ggg ggt ctc      960
Asp Ser Cys Gly Thr Ser Lys Trp Gly Glu Phe Gly Glu Gly Gly Leu
305                 310                 315                 320

tta tgg gga gaa tgt agt tct aga cat ttt gaa tgg ttt gat ggc agc     1008
Leu Trp Gly Glu Cys Ser Ser Arg His Phe Glu Trp Phe Asp Gly Ser
                325                 330                 335

cct ctc tct gat ctc ttg gtc aag gta aag gag ctt tat ggt ctt gat     1056
Pro Leu Ser Asp Leu Leu Val Lys Val Lys Glu Leu Tyr Gly Leu Asp
            340                 345                 350

gat gag gtt act ttt cga aac aca acc gta tct tcg aga cat agg gct     1104
Asp Glu Val Thr Phe Arg Asn Thr Thr Val Ser Ser Arg His Arg Ala
        355                 360                 365

cga cct tta acc ctt gga aca tct act caa att ggt gcc att cat acg     1152
Arg Pro Leu Thr Leu Gly Thr Ser Thr Gln Ile Gly Ala Ile His Thr
    370                 375                 380

gaa gga ata cct tct ttg tta aag gtc tta ctt tca cca agt tgc aat     1200
Glu Gly Ile Pro Ser Leu Leu Lys Val Leu Leu Ser Pro Ser Cys Asn
385                 390                 395                 400

gga tta ccg gtt ctg tat ata agg aat ctt ctc ttg aat cct cct tct     1248
Gly Leu Pro Val Leu Tyr Ile Arg Asn Leu Leu Leu Asn Pro Pro Ser
                405                 410                 415

tat gag atc gca tcc aaa att cag gaa aca tgc aaa ctt atg agc agt     1296
Tyr Glu Ile Ala Ser Lys Ile Gln Glu Thr Cys Lys Leu Met Ser Ser
            420                 425                 430

tta acg tgc tca att cca gaa ttt acg tgt gtt tct tca gca aag ctt     1344
Leu Thr Cys Ser Ile Pro Glu Phe Thr Cys Val Ser Ser Ala Lys Leu
        435                 440                 445

gta aag cta ctt gag tgg agg gag gtc aac cat atg gaa ttt tgt aga     1392
Val Lys Leu Leu Glu Trp Arg Glu Val Asn His Met Glu Phe Cys Arg
    450                 455                 460

ata aag aat gtg ctt gat gag att ttg cat atg tac aaa acc tct gag     1440
Ile Lys Asn Val Leu Asp Glu Ile Leu His Met Tyr Lys Thr Ser Glu
465                 470                 475                 480

ctc aat gaa ata ttg aaa aat tta att gat cca aca tgg gcg aca act     1488
Leu Asn Glu Ile Leu Lys Asn Leu Ile Asp Pro Thr Trp Ala Thr Thr
                485                 490                 495

ggg tta gac atc gac ttt gaa aca ctg gtt tct gga tgt gaa gtt gca     1536
Gly Leu Asp Ile Asp Phe Glu Thr Leu Val Ser Gly Cys Glu Val Ala
            500                 505                 510

tct agt aag atc agt gaa ata atc tct ctg gat ggt ggg aat gat cag     1584
Ser Ser Lys Ile Ser Glu Ile Ile Ser Leu Asp Gly Gly Asn Asp Gln
        515                 520                 525
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aaa atc aac tct tta tct att att cct tat gaa ttt ttt gaa gat acg      1632
Lys Ile Asn Ser Leu Ser Ile Ile Pro Tyr Glu Phe Phe Glu Asp Thr
    530                 535                 540

gag tct aaa tgg aaa ggt cga ata aaa aga gtc cat ata gat gag gtg      1680
Glu Ser Lys Trp Lys Gly Arg Ile Lys Arg Val His Ile Asp Glu Val
545                 550                 555                 560

ttt aca gca gtg caa aaa gca gct gag gtc ttg cac ata gct gtc act      1728
Phe Thr Ala Val Gln Lys Ala Ala Glu Val Leu His Ile Ala Val Thr
                565                 570                 575

gaa gat ttt gtt cct gtt gtt tct aga gta aag gct act ata gcc cca      1776
Glu Asp Phe Val Pro Val Val Ser Arg Val Lys Ala Thr Ile Ala Pro
            580                 585                 590

ctt gga ggt cct agg gga gaa att tct tat gct cgt gag cat gag gca      1824
Leu Gly Gly Pro Arg Gly Glu Ile Ser Tyr Ala Arg Glu His Glu Ala
        595                 600                 605

gtt tgg ttc aga ggc aaa cgc ttt acg ccg agt ttg tgg tct ggt agc      1872
Val Trp Phe Arg Gly Lys Arg Phe Thr Pro Ser Leu Trp Ser Gly Ser
    610                 615                 620

cct ggg gag gaa caa att aaa cag ctt agg cat gct tta gat tct aaa      1920
Pro Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys
625                 630                 635                 640

ggt aaa agg gta ggg gag gaa tgg ttt act aca ccg aag gtt gag gct      1968
Gly Lys Arg Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ala
                645                 650                 655

gca tta aca agg tac cat gaa gca aat gcc aag gca aca gaa cga gtt      2016
Ala Leu Thr Arg Tyr His Glu Ala Asn Ala Lys Ala Thr Glu Arg Val
            660                 665                 670

ttg gaa att tta agg gaa ctc gct act gaa ttg cat tac agt ata aac      2064
Leu Glu Ile Leu Arg Glu Leu Ala Thr Glu Leu His Tyr Ser Ile Asn
        675                 680                 685

att ctt gtc ttt tca tcc acg ttg ctt gtt att acc aaa gct tta ttc      2112
Ile Leu Val Phe Ser Ser Thr Leu Leu Val Ile Thr Lys Ala Leu Phe
    690                 695                 700

gct cat gca agt gaa ggg aga aga agg aga tgg gtt ttt cca aca ctt      2160
Ala His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu
705                 710                 715                 720

gca gaa tcg aat ggg ttt gag gat gtg aaa tct tcg gac aaa atc cat      2208
Ala Glu Ser Asn Gly Phe Glu Asp Val Lys Ser Ser Asp Lys Ile His
                725                 730                 735

ggg atg aag ata gtt ggt tta gca cct tat tgg ttc cac ata gca gaa      2256
Gly Met Lys Ile Val Gly Leu Ala Pro Tyr Trp Phe His Ile Ala Glu
            740                 745                 750

ggt att gtg cgt aat gat gtt gat atg caa tca tta ttt ctt ttg aca      2304
Gly Ile Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr
        755                 760                 765

gga cca aat ggt ggt ggg aaa tca agt tta ctt cgt tca att tgt gct      2352
Gly Pro Asn Gly Gly Gly Lys Ser Ser Leu Leu Arg Ser Ile Cys Ala
    770                 775                 780
```

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gcc gca tta ctt ggt ata tgt ggg ctc atg gtt cct gca gaa tct gcc     2400
Ala Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala
785                 790                 795                 800

gtg att cct tat ttt gac tcc atc acg ctt cat atg aag tcg tat gat     2448
Val Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp
                805                 810                 815

agt cca gct gat aaa aag agt tcc ttt cag gtg gaa atg tca gaa ctt     2496
Ser Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu
            820                 825                 830

aga tcc atc att ggc gga acc acc aaa agg agc ctt gta ctt gtt gat     2544
Arg Ser Ile Ile Gly Gly Thr Thr Lys Arg Ser Leu Val Leu Val Asp
        835                 840                 845

gaa att tgc cga gga aca gaa act gca aaa ggg act tgt att gct ggt     2592
Glu Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly
    850                 855                 860

agt atc att gaa act cta gaa aga att ggt tgt ctg ggt gtt gtg tcc     2640
Ser Ile Ile Glu Thr Leu Glu Arg Ile Gly Cys Leu Gly Val Val Ser
865                 870                 875                 880

act cac ttg cat gga ata ttt act ttg ccc ctc aac atc aaa agc act     2688
Thr His Leu His Gly Ile Phe Thr Leu Pro Leu Asn Ile Lys Ser Thr
                885                 890                 895

gtg cac aaa gca atg ggc aca acg tgc att gat gga caa ata ctt cct     2736
Val His Lys Ala Met Gly Thr Thr Cys Ile Asp Gly Gln Ile Leu Pro
            900                 905                 910

aca tgg aag ctg aca gat gga gtc tgt aaa gaa agt ctt gct ttt gaa     2784
Thr Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu
        915                 920                 925

act gcc att agg gaa gga att cct gag cct att ata aga aga gct gaa     2832
Thr Ala Ile Arg Glu Gly Ile Pro Glu Pro Ile Ile Arg Arg Ala Glu
    930                 935                 940

tgt ctt tat aag tca gtt tat gca gag gaa aat ttc cca aat gaa gag     2880
Cys Leu Tyr Lys Ser Val Tyr Ala Glu Glu Asn Phe Pro Asn Glu Glu
945                 950                 955                 960

aag ttt tct act tgc aac aat ttg aat aat ttg aat aca aca agt ctt     2928
Lys Phe Ser Thr Cys Asn Asn Leu Asn Asn Leu Asn Thr Thr Ser Leu
                965                 970                 975

tat tct aaa ggg ttc tta tca gga gct aat caa atg gaa ggt ttt cgc     2976
Tyr Ser Lys Gly Phe Leu Ser Gly Ala Asn Gln Met Glu Gly Phe Arg
            980                 985                 990

cag gaa gtt gaa aga gct att act  gtg ata tgc cag gat  tat ata atg   3024
Gln Glu Val Glu Arg Ala Ile Thr  Val Ile Cys Gln Asp  Tyr Ile Met
        995                 1000                1005

gaa cgg  aaa aac aaa aag att  gca ttg gag ctt cct  gag ata aaa      3069
Glu Arg  Lys Asn Lys Lys Ile  Ala Leu Glu Leu Pro  Glu Ile Lys
    1010                1015                1020

tgt ctc  cta atc ggt aag agg  gag cag cca cct cca  tct gtt gta      3114
Cys Leu  Leu Ile Gly Lys Arg  Glu Gln Pro Pro Pro  Ser Val Val
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    1025                1030                1035

ggt tct  tca agc gtc tat gtg  att ttc acg cca gat  aag aaa ctc      3159
Gly Ser  Ser Ser Val Tyr Val  Ile Phe Thr Pro Asp  Lys Lys Leu
    1040                1045                1050

tac gta  gga gag acg gat gat  cta gag ggc cgg gtt  cga aga cat      3204
Tyr Val  Gly Glu Thr Asp Asp  Leu Glu Gly Arg Val  Arg Arg His
    1055                1060                1065

aga ttg  aaa gaa ggt atg gat  gaa gca tca ttt ctt  tat ttt ctt      3249
Arg Leu  Lys Glu Gly Met Asp  Glu Ala Ser Phe Leu  Tyr Phe Leu
    1070                1075                1080

gtt ccg  gga aaa agc ttg gca  tgc caa ttt gaa tct  ctg ctc atc      3294
Val Pro  Gly Lys Ser Leu Ala  Cys Gln Phe Glu Ser  Leu Leu Ile
    1085                1090                1095

aac cag  ctt tct agt caa ggc  ttc caa ctg agc aac  atg gct gat      3339
Asn Gln  Leu Ser Ser Gln Gly  Phe Gln Leu Ser Asn  Met Ala Asp
    1100                1105                1110

ggt aaa  cat agg aat ttt ggc  act tcc aac ctc tat  gca taa         3381
Gly Lys  His Arg Asn Phe Gly  Thr Ser Asn Leu Tyr  Ala
    1115                1120                1125


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<213>  Phaseolus vulgaris

<400>  47

Met Tyr Arg Ala Val Thr Arg Asn Val Ala Val Phe Leu Pro Arg Cys
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Arg Ser Leu Ser His Phe Ser His Ser Leu Phe Pro Phe Phe Ile Ser
            20                  25                  30


Ser Leu Pro Ser Arg Phe Leu Arg Ile Asn Gly Arg Val Lys Asn Val
        35                  40                  45


Ser Thr Tyr Met Asp Asn Asn Arg Val Ser Arg Gly Ser Ser Arg Thr
    50                  55                  60


Thr Lys Lys Pro Lys Val Pro Asn Asn Val Leu Asp Asp Lys Asp Leu
65                  70                  75                  80


Pro His Ile Ser Trp Trp Lys Glu Arg Leu Gln Met Cys Lys Lys Phe
                85                  90                  95


Ser Thr Val Gln Leu Ile Gln Arg Leu Glu Phe Ser Asn Leu Leu Gly
            100                 105                 110


Leu Asp Ser Lys Leu Lys Asn Gly Ser Val Lys Glu Gly Thr Leu Asn
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115 120 125

Trp Glu Met Leu Gln Phe Lys Ser Lys Phe Pro Arg Gln Val Leu Leu
130 135 140

Cys Arg Val Gly Glu Phe Tyr Glu Ala Trp Gly Ile Asp Ala Cys Val
145 150 155 160

Leu Val Glu Tyr Ala Gly Leu Asn Pro Cys Gly Gly Leu Gln Ser Asp
165 170 175

Ser Val Pro Arg Ala Gly Cys Pro Val Val Asn Leu Arg Gln Thr Leu
180 185 190

Asp Asp Leu Thr Gln Asn Gly Tyr Ser Val Cys Ile Ile Glu Glu Val
195 200 205

Gln Gly Pro Thr Gln Ala Arg Ser Arg Lys Arg Arg Phe Ile Ser Gly
210 215 220

His Ala His Pro Gly Asn Pro Tyr Val Tyr Gly Leu Ala Ala Val Asp
225 230 235 240

His Asp Leu Asn Phe Pro Glu Pro Met Pro Val Ile Gly Ile Ser His
245 250 255

Ser Ala Arg Gly Tyr Cys Ile Asn Met Val Leu Glu Thr Met Lys Thr
260 265 270

Tyr Ser Tyr Glu Asp Cys Leu Thr Glu Glu Ala Ile Val Thr Lys Leu
275 280 285

Arg Thr Cys Gln Tyr His His Leu Phe Leu His Thr Ser Leu Thr Gln
290 295 300

Asp Ser Cys Gly Thr Ser Lys Trp Gly Glu Phe Gly Glu Gly Gly Leu
305 310 315 320

Leu Trp Gly Glu Cys Ser Ser Arg His Phe Glu Trp Phe Asp Gly Ser
325 330 335

Pro Leu Ser Asp Leu Leu Val Lys Val Lys Glu Leu Tyr Gly Leu Asp
340 345 350

Asp Glu Val Thr Phe Arg Asn Thr Thr Val Ser Ser Arg His Arg Ala
355 360 365

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Arg Pro Leu Thr Leu Gly Thr Ser Thr Gln Ile Gly Ala Ile His Thr
    370                 375                 380

Glu Gly Ile Pro Ser Leu Leu Lys Val Leu Leu Ser Pro Ser Cys Asn
385                 390                 395                 400

Gly Leu Pro Val Leu Tyr Ile Arg Asn Leu Leu Leu Asn Pro Pro Ser
                405                 410                 415

Tyr Glu Ile Ala Ser Lys Ile Gln Glu Thr Cys Lys Leu Met Ser Ser
            420                 425                 430

Leu Thr Cys Ser Ile Pro Glu Phe Thr Cys Val Ser Ser Ala Lys Leu
        435                 440                 445

Val Lys Leu Leu Glu Trp Arg Glu Val Asn His Met Glu Phe Cys Arg
    450                 455                 460

Ile Lys Asn Val Leu Asp Glu Ile Leu His Met Tyr Lys Thr Ser Glu
465                 470                 475                 480

Leu Asn Glu Ile Leu Lys Asn Leu Ile Asp Pro Thr Trp Ala Thr Thr
                485                 490                 495

Gly Leu Asp Ile Asp Phe Glu Thr Leu Val Ser Gly Cys Glu Val Ala
            500                 505                 510

Ser Ser Lys Ile Ser Glu Ile Ile Ser Leu Asp Gly Gly Asn Asp Gln
        515                 520                 525

Lys Ile Asn Ser Leu Ser Ile Ile Pro Tyr Glu Phe Phe Glu Asp Thr
    530                 535                 540

Glu Ser Lys Trp Lys Gly Arg Ile Lys Arg Val His Ile Asp Glu Val
545                 550                 555                 560

Phe Thr Ala Val Gln Lys Ala Ala Glu Val Leu His Ile Ala Val Thr
                565                 570                 575

Glu Asp Phe Val Pro Val Val Ser Arg Val Lys Ala Thr Ile Ala Pro
            580                 585                 590

Leu Gly Gly Pro Arg Gly Glu Ile Ser Tyr Ala Arg Glu His Glu Ala
        595                 600                 605

Val Trp Phe Arg Gly Lys Arg Phe Thr Pro Ser Leu Trp Ser Gly Ser
    610                 615                 620
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Pro Gly Glu Glu Gln Ile Lys Gln Leu Arg His Ala Leu Asp Ser Lys
625                 630                 635                 640

Gly Lys Arg Val Gly Glu Glu Trp Phe Thr Thr Pro Lys Val Glu Ala
                645                 650                 655

Ala Leu Thr Arg Tyr His Glu Ala Asn Ala Lys Ala Thr Glu Arg Val
            660                 665                 670

Leu Glu Ile Leu Arg Glu Leu Ala Thr Glu Leu His Tyr Ser Ile Asn
        675                 680                 685

Ile Leu Val Phe Ser Ser Thr Leu Leu Val Ile Thr Lys Ala Leu Phe
    690                 695                 700

Ala His Ala Ser Glu Gly Arg Arg Arg Arg Trp Val Phe Pro Thr Leu
705                 710                 715                 720

Ala Glu Ser Asn Gly Phe Glu Asp Val Lys Ser Ser Asp Lys Ile His
                725                 730                 735

Gly Met Lys Ile Val Gly Leu Ala Pro Tyr Trp Phe His Ile Ala Glu
            740                 745                 750

Gly Ile Val Arg Asn Asp Val Asp Met Gln Ser Leu Phe Leu Leu Thr
        755                 760                 765

Gly Pro Asn Gly Gly Gly Lys Ser Ser Leu Leu Arg Ser Ile Cys Ala
    770                 775                 780

Ala Ala Leu Leu Gly Ile Cys Gly Leu Met Val Pro Ala Glu Ser Ala
785                 790                 795                 800

Val Ile Pro Tyr Phe Asp Ser Ile Thr Leu His Met Lys Ser Tyr Asp
                805                 810                 815

Ser Pro Ala Asp Lys Lys Ser Ser Phe Gln Val Glu Met Ser Glu Leu
            820                 825                 830

Arg Ser Ile Ile Gly Gly Thr Thr Lys Arg Ser Leu Val Leu Val Asp
        835                 840                 845

Glu Ile Cys Arg Gly Thr Glu Thr Ala Lys Gly Thr Cys Ile Ala Gly
    850                 855                 860

Ser Ile Ile Glu Thr Leu Glu Arg Ile Gly Cys Leu Gly Val Val Ser
865                 870                 875                 880
```

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Thr His Leu His Gly Ile Phe Thr Leu Pro Leu Asn Ile Lys Ser Thr
                885                 890                 895

Val His Lys Ala Met Gly Thr Thr Cys Ile Asp Gly Gln Ile Leu Pro
            900                 905                 910

Thr Trp Lys Leu Thr Asp Gly Val Cys Lys Glu Ser Leu Ala Phe Glu
        915                 920                 925

Thr Ala Ile Arg Glu Gly Ile Pro Glu Pro Ile Ile Arg Arg Ala Glu
    930                 935                 940

Cys Leu Tyr Lys Ser Val Tyr Ala Glu Glu Asn Phe Pro Asn Glu Glu
945                 950                 955                 960

Lys Phe Ser Thr Cys Asn Asn Leu Asn Asn Leu Asn Thr Thr Ser Leu
                965                 970                 975

Tyr Ser Lys Gly Phe Leu Ser Gly Ala Asn Gln Met Glu Gly Phe Arg
            980                 985                 990

Gln Glu Val Glu Arg Ala Ile Thr  Val Ile Cys Gln Asp  Tyr Ile Met
        995                 1000                1005

Glu Arg  Lys Asn Lys Lys Ile  Ala Leu Glu Leu Pro  Glu Ile Lys
    1010                1015                1020

Cys Leu  Leu Ile Gly Lys Arg  Glu Gln Pro Pro Pro  Ser Val Val
    1025                1030                1035

Gly Ser  Ser Ser Val Tyr Val  Ile Phe Thr Pro Asp  Lys Lys Leu
    1040                1045                1050

Tyr Val  Gly Glu Thr Asp Asp  Leu Glu Gly Arg Val  Arg Arg His
    1055                1060                1065

Arg Leu  Lys Glu Gly Met Asp  Glu Ala Ser Phe Leu  Tyr Phe Leu
    1070                1075                1080

Val Pro  Gly Lys Ser Leu Ala  Cys Gln Phe Glu Ser  Leu Leu Ile
    1085                1090                1095

Asn Gln  Leu Ser Ser Gln Gly  Phe Gln Leu Ser Asn  Met Ala Asp
    1100                1105                1110

Gly Lys  His Arg Asn Phe Gly  Thr Ser Asn Leu Tyr  Ala
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ggccatggaa acatcacttg acgtcttc 28

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agtggttatt tgggt 15

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gatgttgcag tttaa 15

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tactcaaaga ttg 13

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Leu Leu Phe Tyr Arg Met Gly Asp Phe Tyr Glu Leu Phe Tyr Asp Asp
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Ala

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Ala

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Val Val Phe Phe Lys Met Ala Lys Phe Tyr Glu Leu Phe Glu Met Asp
1 5 10 15

Ala

<210> 59
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<213> Arabadopsis thaliana

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Val Leu Leu Cys Arg Val Gly Glu Phe Tyr Glu Ala Ile Gly Ile Asp
1 5 10 15

Ala

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Leu Leu Phe Tyr Arg Met Gly Asp Phe Tyr Glu Leu Phe Tyr Asp Asp
1 5 10 15

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<400> 61

Asp Lys Pro Gly Ile Arg Ile Thr Glu Gly Arg His Pro Val Val Glu
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Gln Val Leu Asn Glu Pro Phe Ile Ala Asn Pro Leu Asn Asn Ser Pro
20 25 30

Gln Arg Arg Met Leu Ile Ile Thr Gly Pro Asn Met Gly Gly Lys Ser
35 40 45

Thr Tyr Met Arg Gln Thr Ala Leu Ile Ala Leu Met Ala Tyr Ile Gly
50 55 60

Ser Tyr Val Pro Ala Gln Lys Val Glu Ile Gly Pro Ile Asp Arg Ile
65 70 75 80

Phe Thr Arg Val Gly Ala Ala Asp Asp Leu Ala Ser Gly Arg Ser Thr
85 90 95

Phe Met Val Glu Met Thr Glu Thr Ala Asn Ile Leu His Asn Ala Thr
100 105 110

Glu Tyr Ser Leu Val Leu Met Asp Glu Ile Gly Arg Gly Thr Ser Thr
115 120 125

Tyr Asp Gly Leu Ser Leu Ala Trp Cys Ala Glu Asn Leu Ala Asn Lys
130 135 140

Ile Lys Ala Leu Thr Leu Phe Ala Thr His Tyr Phe Glu Leu Thr Gln
145 150 155 160

Leu Pro Glu Lys Met Glu Gly Glx Val Ala Asn Val His
165 170

<210> 62
<211> 177
<212> PRT
<213> Saccharomyces cerevisiae

<400> 62

Glu Ser Asn Lys Leu Glu Val Val Asn Gly Arg His Leu Met Val Glu
1 5 10 15

Glu Gly Leu Ser Ala Arg Ser Leu Glu Thr Phe Thr Ala Asn Asn Cys
20 25 30

Glu Leu Ala Lys Asp Asn Leu Trp Val Ile Thr Gly Pro Asn Met Gly
35 40 45

Gly Lys Ser Thr Phe Leu Arg Gln Asn Ala Ile Ile Val Ile Leu Ala
50 55 60

Gln Ile Gly Cys Phe Val Pro Cys Ser Lys Ala Arg Val Gly Ile Val
65 70 75 80

Asp Lys Leu Phe Ser Arg Val Gly Ser Ala Asp Asp Leu Tyr Asn Glu
85 90 95

Met Ser Thr Phe Met Val Glx Glu Met Ile Glu Thr Ser Phe Ile Leu
100 105 110

Gln Gly Ala Thr Glu Arg Ser Leu Ala Ile Leu Asp Glu Ile Gly Arg
115 120 125

Gly Thr Ser Gly Lys Glu Gly Ile Ser Ile Ala Tyr Ala Thr Leu Lys
130 135 140

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Tyr Leu Leu Glu Asn Asn Gln Cys Arg Thr Leu Phe Ala Thr His Phe
145                 150                 155                 160

Gly Gln Glu Leu Lys Gln Ile Asp Asn Lys Cys Ser Lys Gly Met Ser
                165                 170                 175

Glu
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Gly Asp Ser Leu Gly Arg Gly Ser Phe Val Pro Asn Asn Val Lys Ile
            20                  25                  30

Gly Gly Ala Glu Lys Ala Ser Phe Ile Leu Leu Thr Gly Pro Asn Met
        35                  40                  45

Gly Gly Lys Ser Thr Leu Leu Arg Gln Val Cys Leu Ala Val Ile Leu
    50                  55                  60

Ala Gln Ile Gly Ala Asp Val Pro Ala Glu Thr Phe Glu Val Ser Pro
65                  70                  75                  80

Val Asp Lys Ile Cys Val Arg Met Gly Ala Lys Asp His Ile Met Ala
                85                  90                  95

Gly Gln Ser Thr Phe Leu Thr Glu Leu Ser Glu Thr Ala Val Met Leu
            100                 105                 110

Thr Ser Ala Thr Arg Asn Ser Leu Val Val Leu Asp Glu Leu Gly Arg
        115                 120                 125

Gly Thr Ala Thr Ser Asp Gly Gln Ala Ile Ala Glu Ser Val Leu Glu
    130                 135                 140

His Phe Ile Glu Lys Val Gln Cys Arg Gly Phe Phe Ser Thr His Tyr
145                 150                 155                 160

His Arg Leu Ser Val Asp Tyr Gln Thr Asn Pro Lys Val Ser Leu Cys
                165                 170                 175
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His

<210> 64
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<213> Arabadopsis thaliana

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Leu Asp Glu Gly Ala Lys Pro Leu Asp Gly Ala Ser Arg Met Lys Leu
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Val Ser Gln Ala Thr Ser Arg Ser Leu Val Leu Ile Asp Glu Ile Cys
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His Ala His Pro Gly Ser Pro Tyr Val Tyr Gly Leu Ala Val Asp His
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Glu Leu Leu Lys Val Lys Glu Leu Tyr Gly Leu Asp Asp Glu Val Thr
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Phe Arg Asn Val Thr Val Ser Ser Arg Pro Arg Pro Leu His Leu Gly
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Asp Leu Leu Leu Asn Pro Pro Ser Tyr Glu Ile Ala Ser Lys Ile Gln
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Glu Thr Cys Lys Leu Met Ser Ser Val Thr Cys Ser Ile Pro Glu Phe
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Asn His Ile Glu Phe Cys Arg Ile Lys Asn Val Leu Asp Glu Ile Leu
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Tyr Ser Asn Leu Leu Gly Leu Asp Pro Ser Leu Arg Asn Gly Ser Leu
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Pro Arg Glu Val Leu Leu Cys Arg Val Gly Glu Phe Tyr Glu Ala Ile
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Xaa Arg Phe Ile Ser Gly His Ala His Pro Gly Ser Pro Tyr Val Tyr
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